```
=> d his nofile

     (FILE 'HOME' ENTERED AT 09:54:26 ON 05 SEP 2006)

     FILE 'CAPLUS' ENTERED AT 09:54:40 ON 05 SEP 2006
                SET LINE 250
                SET DETAIL OFF
                E US1999-235416/AP,PRN 25
                SET LINE LOGIN
                SET DETAIL LOGIN
L1            1 SEA ABB=ON  US99-235416/PRN
                D SCAN
L2           45 SEA ABB=ON  SAKOWICZ R?/AU
L3         1091 SEA ABB=ON  GOLDSTEIN L?/AU
L4           61 SEA ABB=ON  (THERMOMYCES LANUGINOSUS/OBI OR TL/OBI)(W)GAMMA/OBI

                E TEST KITS+ALL/CT
L5        17063 SEA ABB=ON  TEST KITS/CT
L6            9 SEA ABB=ON  (L2 AND L3) OR ((L2 OR L3) AND L4)
L7         1841 SEA ABB=ON  KINESINS/CT
L8            2 SEA ABB=ON  THERMOMYCES LANUGINOSUS/CT(L)GAMMA/OBI
L9        20619 SEA ABB=ON  MICROTUBULE#/OBI
L10        3352 SEA ABB=ON  MOTOR/OBI(L)PROTEIN#/OBI

     FILE 'REGISTRY' ENTERED AT 09:59:03 ON 05 SEP 2006
                E PROTEIN KINASE/CN
L11           1 SEA ABB=ON  "PROTEIN KINASE"/CN

     FILE 'REGISTRY' ENTERED AT 09:59:23 ON 05 SEP 2006
                D IDE

     FILE 'CAPLUS' ENTERED AT 09:59:35 ON 05 SEP 2006
L12       97768 SEA ABB=ON  L11 OR PROTEIN KINASE#/OBI
L13           0 SEA ABB=ON  L8 NOT L4
L14           1 SEA ABB=ON  L4 AND (L5 OR L7 OR L9 OR L10 OR L12)
L15         220 SEA ABB=ON  L7 AND L9 AND L10
L16         161 SEA ABB=ON  L9(L)L10 AND L7
L17          48 SEA ABB=ON  END DIRECT?/OBI
L18           3 SEA ABB=ON  L15 AND L17
                E SCREENING/CT
L19       42502 SEA ABB=ON  L12(L)(MODULAT?/OBI OR INHIBIT?/OBI OR ACTIVAT?/OBI
                )
L20          11 SEA ABB=ON  L15 AND L19
L21           0 SEA ABB=ON  L16 AND L19
                D QUE L20
                D SCAN TI L20
L22           1 SEA ABB=ON  MAP/TI AND L20
                D SCAN
L23         477 SEA ABB=ON  L19(L)ANST/RL
L24           3 SEA ABB=ON  L15 AND L23
L25         233 SEA ABB=ON  L19 AND L5
                D SCA L1
L26          20 SEA ABB=ON  L7 AND L25
                D QUE
L27           8 SEA ABB=ON  L7 AND L25 AND L23
                D SCAN TI

     FILE 'WPIX' ENTERED AT 10:38:16 ON 05 SEP 2006
L28          36 SEA ABB=ON  SAKOWICZ R?/AU
L29          64 SEA ABB=ON  GOLDSTEIN L?/AU
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L30           1 SEA ABB=ON  (THERMOMYCES LANUGINOSUS/BI,ABEX OR TL/BI,ABEX)(A)G
                AMMA/BI,ABEX
                D TRIAL
L31           3 SEA ABB=ON  L28 AND L29
                D TRIAL 1-3
L32         252 SEA ABB=ON  KINESIN#/BI,ABEX
L33         811 SEA ABB=ON  MICROTUBULE#/BI,ABEX OR MICRO TUBULE#/BI,ABEX
L34         120 SEA ABB=ON  MOTOR PROTEIN#/BI,ABEX
L35        1863 SEA ABB=ON  END DIRECT?/BI,ABEX
L36        4006 SEA ABB=ON  PROTEIN KINASE#/BI,ABEX
L37         105 SEA ABB=ON  L32 AND (L33 OR L34 OR L35)
L38          54 SEA ABB=ON  L32 AND L33 AND L34
L39           3 SEA ABB=ON  L32 AND L33 AND L34 AND L35
L40           1 SEA ABB=ON  L37 AND L36
L41        2492 SEA ABB=ON  L36(3A)(MODULAT?/BI,ABEX OR INHIBIT?/BI,ABEX OR
                ACTIVAT?/BI,ABEX)
L42           3 SEA ABB=ON  L32 AND L41
                D TRIAL 1-3
L43      302435 SEA ABB=ON  SCREEN?/BI,ABEX
L44        1372 SEA ABB=ON  DRUG#/BI,ABEX(2A)CANDIDATE#/BI,ABEX
L45         484 SEA ABB=ON  L41 AND (L43 OR L44)
L46          15 SEA ABB=ON  L41 AND L43 AND L44
                D TRIAL 1-5
                D QUE
L47          45 SEA ABB=ON  L41 AND (L33 OR L34 OR L35)
L48           9 SEA ABB=ON  L41 AND (L33 OR L34 OR L35) AND (L43 OR L44)
                D TRIAL 1-3
                D TRIAL L31 1-3

     FILE 'STNGUIDE' ENTERED AT 10:52:47 ON 05 SEP 2006

     FILE 'WPIX' ENTERED AT 10:58:19 ON 05 SEP 2006
L49       11026 SEA ABB=ON  L43(2A)(DRUG#/BI,ABEX OR COMPOUND#/BI,ABEX)
L50           2 SEA ABB=ON  L41 AND (L33 OR L34 OR L35) AND (L44 OR L49)
                D TRIAL 1-2
                D KWIC 1-2
L51          38 SEA ABB=ON  L41(S)((L44 OR L49))
L52          19 SEA ABB=ON  L41(10A)((L44 OR L49))
L53          15 SEA ABB=ON  L41(5A)((L44 OR L49))
L54           0 SEA ABB=ON  L51 AND (L33 OR L34 OR L35)

     FILE 'STNGUIDE' ENTERED AT 11:01:44 ON 05 SEP 2006

     FILE 'WPIX' ENTERED AT 11:02:37 ON 05 SEP 2006
L55       50839 SEA ABB=ON  ASSAY#/BI,ABEX
L56        3543 SEA ABB=ON  L43(3A)L55
L57          26 SEA ABB=ON  L56 AND (L49 OR L44) AND L41
L58           1 SEA ABB=ON  L57 AND (L33 OR L34 OR L35)
L59           2 SEA ABB=ON  L56 (S) (L49 OR L44) (S) L41

     INDEX '1MOBILITY, 2MOBILITY, ABI-INFORM, ADISCTI, AEROSPACE, AGRICOLA,
     ALUMINIUM, ANABSTR, ANTE, APOLLIT, AQUALINE, AQUASCI, AQUIRE, BABS,
     BIBLIODATA, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA,
     CAOLD, CAPLUS, CASREACT, CBNB, CEABA-VTB, CERAB, ...' ENTERED AT 11:05:41
     ON 05 SEP 2006
               SEA (THERMOMYCES LANUGINOSUS OR TL)(A)GAMMA
              ---------
               8   FILE AEROSPACE
               1   FILE AGRICOLA
              11   FILE ANABSTR
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                1   FILE AQUASCI
                3   FILE BIOENG
               14   FILE BIOSIS
                2   FILE BIOTECHNO
                4   FILE CABA
                1   FILE CAOLD
               63   FILE CAPLUS
                1   FILE CIVILENG
               46   FILE COMPENDEX
                2   FILE COMPUSCIENCE
                1   FILE CONFSCI
                1   FILE DDFU
                7   FILE DGENE
                5   FILE DISSABS
                1   FILE DRUGU
                2   FILE EMBAL
               16   FILE EMBASE
              150   FILE ENERGY
                1   FILE ENVIROENG
                9   FILE EPFULL
                9   FILE ESBIOBASE
                2   FILE GBFULL
                2   FILE GENBANK
                1   FILE GEOREF
                3   FILE HEALSAFE
                6   FILE IFIPAT
              152   FILE INIS
                4   FILE INPADOC
              176   FILE INSPEC
               10   FILE INSPHYS
                1   FILE JAPIO
               16   FILE JICST-EPLUS
                3   FILE LIFESCI
                3   FILE MECHENG
               11   FILE MEDLINE
                6   FILE METADEX
               33   FILE NTIS
               21   FILE PASCAL
                9   FILE PATDPAFULL
               12   FILE PCTFULL
                5   FILE POLLUAB
               58   FILE SCISEARCH
                1   FILE SOLIDSTATE
                6   FILE TEMA
               21   FILE TOXCENTER
                1   FILE TULSA
                1   FILE ULIDAT
               19   FILE USPATFULL
                3   FILE USPAT2
                1   FILE WPIDS
                1   FILE WPINDEX
L60              QUE ABB=ON  (THERMOMYCES LANUGINOSUS OR TL)(A) GAMMA
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     FILE 'STNGUIDE' ENTERED AT 11:10:58 ON 05 SEP 2006

     FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS,
     ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED
     AT 11:15:21 ON 05 SEP 2006
L61          138 SEA ABB=ON  SAKOWICZ R?/AU
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L62        4782 SEA ABB=ON  GOLDSTEIN L?/AU
L63         147 SEA ABB=ON  (THERMOMYCES LANUGINOSUS OR TL)(A) GAMMA
L64       13861 SEA ABB=ON  KINESIN#
L65      132140 SEA ABB=ON  MICROTUBULE# OR MICRO TUBULE#
L66        7756 SEA ABB=ON  MOTOR PROTEIN#
L67        2654 SEA ABB=ON  END DIRECT?
L68          40 SEA ABB=ON  (L61 AND L62) OR ((L61 OR L62) AND L63)
L69          22 DUP REM L68 (18 DUPLICATES REMOVED)
                    ANSWERS '1-2' FROM FILE DRUGU
                    ANSWER '3' FROM FILE PASCAL
                    ANSWERS '4-5' FROM FILE BIOTECHNO
                    ANSWERS '6-17' FROM FILE BIOSIS
                    ANSWER '18' FROM FILE LIFESCI
                    ANSWERS '19-20' FROM FILE CONFSCI
                    ANSWERS '21-22' FROM FILE SCISEARCH
L70      567385 SEA ABB=ON  PROTEIN KINASE#
L71           3 SEA ABB=ON  L63 AND (L64 OR L65 OR L66 OR L67 OR L70)
L72         377 SEA ABB=ON  L64 AND L65 AND L66 AND L67
L73          83 SEA ABB=ON  L64 AND L65 (5A) L66 (5A) L67
L74          12 SEA ABB=ON  L64 (3A) L65 (3A) L66 (3A) L67
L75          20 SEA ABB=ON  L64 (5A) L65 (5A) L66 (5A) L67
L76      262577 SEA ABB=ON  L70(3A)((MODULAT? OR INHIBIT? OR ACTIVAT?))
L77        2376 SEA ABB=ON  (SCREEN? OR CANDIDATE#)(3A)(DRUG# OR COMPOUND#)(5A)
                  ASSAY?
L78           0 SEA ABB=ON  L76 (S) L77 AND (L64 OR L65 OR L66 OR L67)
L79          12 SEA ABB=ON  L76 (S) L77

     FILE 'MEDLINE' ENTERED AT 11:23:32 ON 05 SEP 2006
L80          13 SEA ABB=ON  SAKOWICZ R?/AU
L81        1168 SEA ABB=ON  GOLDSTEIN L?/AU
L82          11 SEA ABB=ON  (THERMOMYCES LANUGINOSUS OR TL)(A)GAMMA
L83           4 SEA ABB=ON  (L80 AND L81) OR ((L80 OR L81) AND L82)
                  D TRIAL 1-4
                  E KINESIN+ALL/CT
L84        2094 SEA ABB=ON  KINESIN/CT
                  E MICROTUBULES+ALL/CT
L85       17967 SEA ABB=ON  MICROTUBULES/CT
L86       76212 SEA ABB=ON  ENZYME INHIBITORS/CT
                  E MOTOR PROTEIN/CT
L87        1529 SEA ABB=ON  MOTOR PROTEIN#
L88         359 SEA ABB=ON  END DIRECT?
L89           0 SEA ABB=ON  L82 AND (L84 OR L85 OR L86 OR L87 OR L88)
                  D TRIAL L82 1-3
                  D TRIAL L82 4-11
L90         325 SEA ABB=ON  L84 AND L85 AND (L87 OR L88)
L91          34 SEA ABB=ON  L84 AND L85 AND L87 AND L88
L92           9 SEA ABB=ON  L87(8A)L88 AND L84 AND L85
                  E PROTEIN KINASE/CT
                  E E3+ALL
L93      184405 SEA ABB=ON  PROTEIN KINASES+NT/CT
                  E SCREENING/CT
                  E E4+ALL
L94       22924 SEA ABB=ON  DRUG EVALUATION, PRECLINICAL/CT
L95         102 SEA ABB=ON  L93 AND L94 AND L86
L96          64 SEA ABB=ON  L93/MAJ AND L94 AND L86/MAJ
L97          13 SEA ABB=ON  L93/MAJ AND L94(L)MT/CT AND L86/MAJ
                  D TRIAL 1-4
L98        28397 SEA ABB=ON  L93(L)AI/CT
L99         8557 SEA ABB=ON  L98/MAJ
L100       21967 SEA ABB=ON  ENZYME ACTIVATION/CT(L)DE/CT
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L101        189 SEA ABB=ON  L100/MAJ
L102         19 SEA ABB=ON  ((L93/MAJ AND L101) OR L99) AND L94(L)MT/CT
L103       4668 SEA ABB=ON  L94(L)MT/CT
L104       1977 SEA ABB=ON  L103/MAJ
L105         10 SEA ABB=ON  ((L93/MAJ AND L101) OR L99) AND L104
                D TRIAL 1-3
L106          0 SEA ABB=ON  L95 AND L84

     FILE 'EMBASE' ENTERED AT 11:33:37 ON 05 SEP 2006
L107         13 SEA ABB=ON  SAKOWICZ R?/AU
L108        922 SEA ABB=ON  GOLDSTEIN L?/AU
L109         16 SEA ABB=ON  (THERMOMYCES LANUGINOSUS OR TL)(A)GAMMA
L110          5 SEA ABB=ON  (L107 AND L108) OR ((L107 OR L108) AND L109)
                D TRIAL 1-5

     FILE 'STNGUIDE' ENTERED AT 11:34:20 ON 05 SEP 2006

     FILE 'EMBASE' ENTERED AT 12:01:08 ON 05 SEP 2006
L111          5 SEA ABB=ON  (L107 AND L108) OR ((L107 OR L108) AND L109)
                D TRIAL 1-5
L112       2142 SEA ABB=ON  KINESIN/CT
L113       3476 SEA ABB=ON  MICROTUBULE ASSEMBLY/CT
L114        754 SEA ABB=ON  MICROTUBULE PROTEIN/CT
L115      13611 SEA ABB=ON  MICROTUBULE/CT
L116        316 SEA ABB=ON  END DIRECT?
                E MOTOR PROTEIN/CT
                E E3+ALL
L117        569 SEA ABB=ON  MOTOR PROTEIN/CT OR MOLECULAR MOTOR/CT
L118          0 SEA ABB=ON  L109 AND (L112 OR L113 OR L114 OR L115 OR L116 OR
                L117)
L119          7 SEA ABB=ON  L112 AND (L113 OR L114 OR L115) AND L116 AND L117
                E ENZYME ACTIVAT/CT
L120      68045 SEA ABB=ON  ENZYME ACTIVATION/CT
L121       1083 SEA ABB=ON  ENZYME ACTIVATOR/CT
                E ENZYME MODULAT/CT
L122         39 SEA ABB=ON  ENZYME MODULATION/CT
L123      16880 SEA ABB=ON  ENZYME INHIBITOR/CT
L124      89209 SEA ABB=ON  ENZYME INHIBITION/CT
                E PROTEIN KINASE/CT
L125      20757 SEA ABB=ON  PROTEIN KINASE+NT/CT
L126       2690 SEA ABB=ON  L125/MAJ AND (L120 OR L121 OR L122 OR L123 OR
                L124)
L127         31 SEA ABB=ON  L126 AND (L112 OR L113 OR L114 OR L115 OR L116 OR
                L117 OR L109)
L128          4 SEA ABB=ON  GENERAL REVIEW/DT AND L127
                D TRIAL 1-4
                E ENZYME ACTIVITY/CT
L129     221084 SEA ABB=ON  ENZYME ACTIVITY/CT
                E DRUG SCREENING/CT
                E E3+ALL
L130      74504 SEA ABB=ON  DRUG SCREENING/CT
                E E19+ALL
L131      22260 SEA ABB=ON  SCREENING TEST/CT
L132       4100 SEA ABB=ON  L125/MAJ AND (L120 OR L121 OR L122 OR L123 OR L124
                OR L129)
L133         24 SEA ABB=ON  L132 AND (L130 OR L131)
                D TRIAL 1-4
L134       4072 SEA ABB=ON  PROTEIN KINASE INHIBITOR/CT
L135       1431 SEA ABB=ON  L134/MAJ
L136         53 SEA ABB=ON  L135 AND (L130 OR L131)
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L137          71 SEA ABB=ON  L133 OR L136
                 E ANALYTIC METHOD+ALL/CT
                 D QUE L137
L138           1 SEA ABB=ON  L137 AND (L112 OR L113 OR L114 OR L115 OR L116 OR
                 L117 OR L109)

     FILE 'STNGUIDE' ENTERED AT 12:12:41 ON 05 SEP 2006
                 D QUE L105
                 D QUE L92
                 D QUE L79
                 D QUE L75
                 D QUE L58
                 D QUE L59
                 D QUE L40
                 D QUE L24
                 D QUE L27
                 D QUE L18

     FILE 'CAPLUS' ENTERED AT 12:14:47 ON 05 SEP 2006
                 D QUE L1
                 D QUE L6
L139           9 SEA ABB=ON  L1 OR L6

     FILE 'WPIX' ENTERED AT 12:14:49 ON 05 SEP 2006
                 D QUE L31

     FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS,
     ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED
     AT 12:14:50 ON 05 SEP 2006
                 D QUE L68

     FILE 'MEDLINE' ENTERED AT 12:14:52 ON 05 SEP 2006
                 D QUE L83

     FILE 'EMBASE' ENTERED AT 12:14:54 ON 05 SEP 2006
                 D QUE L110

     FILE 'MEDLINE, CAPLUS, WPIX, EMBASE, DRUGU, PASCAL, BIOTECHNO, BIOSIS,
     ESBIOBASE, LIFESCI, CONFSCI, SCISEARCH' ENTERED AT 12:15:12 ON 05 SEP 2006
L140          26 DUP REM L83 L139 L31 L110 L68 (35 DUPLICATES REMOVED)
                       ANSWERS '1-4' FROM FILE MEDLINE
                       ANSWERS '5-10' FROM FILE CAPLUS
                       ANSWERS '11-21' FROM FILE BIOSIS
                       ANSWER '22' FROM FILE LIFESCI
                       ANSWERS '23-24' FROM FILE CONFSCI
                       ANSWERS '25-26' FROM FILE SCISEARCH
                 D IBIB ED ABS 1-26

     FILE 'STNGUIDE' ENTERED AT 12:15:40 ON 05 SEP 2006
                 D QUE L14
                 D QUE L18
                 D QUE L30
                 D QUE L39
                 D QUE L40
                 D QUE L71
                 D QUE L75

     FILE 'CAPLUS' ENTERED AT 12:17:36 ON 05 SEP 2006
                 D QUE L14
L141           0 SEA ABB=ON  L14 NOT L139
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FILE 'WPIX' ENTERED AT 12:17:38 ON 05 SEP 2006
D QUE L30

FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS, ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED AT 12:17:40 ON 05 SEP 2006
D QUE L71
L142 0 SEA ABB=ON L71 NOT L68

FILE 'MEDLINE' ENTERED AT 12:17:48 ON 05 SEP 2006
D QUE L89

FILE 'EMBASE' ENTERED AT 12:17:50 ON 05 SEP 2006
D QUE L118

FILE 'CAPLUS' ENTERED AT 12:19:00 ON 05 SEP 2006
D QUE L14
L143 0 SEA ABB=ON L14 NOT L139

FILE 'WPIX' ENTERED AT 12:19:01 ON 05 SEP 2006
D QUE L30
L144 0 SEA ABB=ON L30 NOT L31

FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS, ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED AT 12:19:04 ON 05 SEP 2006
D QUE L71
L145 0 SEA ABB=ON L71 NOT L68

FILE 'MEDLINE' ENTERED AT 12:19:12 ON 05 SEP 2006
D QUE L89

FILE 'EMBASE' ENTERED AT 12:19:14 ON 05 SEP 2006
D QUE L118

FILE 'STNGUIDE' ENTERED AT 12:19:27 ON 05 SEP 2006

FILE 'CAPLUS' ENTERED AT 12:20:57 ON 05 SEP 2006
D QUE L18
L146 3 SEA ABB=ON L18 NOT L139

FILE 'WPIX' ENTERED AT 12:20:58 ON 05 SEP 2006
D QUE L39
D QUE L40
L147 3 SEA ABB=ON (L39 OR L40) NOT L31

FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS, ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED AT 12:21:01 ON 05 SEP 2006
D QUE L75
L148 20 SEA ABB=ON L75 NOT L68

FILE 'MEDLINE' ENTERED AT 12:21:10 ON 05 SEP 2006
D QUE L92
L149 9 SEA ABB=ON L92 NOT L83

FILE 'EMBASE' ENTERED AT 12:21:12 ON 05 SEP 2006
D QUE L119
L150 7 SEA ABB=ON L119 NOT L110

FILE 'STNGUIDE' ENTERED AT 12:21:21 ON 05 SEP 2006

FILE 'MEDLINE, CAPLUS, WPIX, EMBASE, BIOTECHNO, BIOSIS, ESBIOBASE, LIFESCI, SCISEARCH' ENTERED AT 12:21:44 ON 05 SEP 2006

L151 28 DUP REM L149 L146 L147 L150 L148 (14 DUPLICATES REMOVED)
ANSWERS '1-9' FROM FILE MEDLINE
ANSWERS '10-12' FROM FILE CAPLUS
ANSWERS '13-15' FROM FILE WPIX
ANSWERS '16-21' FROM FILE EMBASE
ANSWERS '22-23' FROM FILE BIOTECHNO
ANSWERS '24-27' FROM FILE BIOSIS
ANSWER '28' FROM FILE LIFESCI
D IALL 1-9
D IBIB ED ABS HITIND 10-12
D IALL ABEQ TECH 13-15
D IALL 16-28

FILE 'STNGUIDE' ENTERED AT 12:22:44 ON 05 SEP 2006

FILE 'CAPLUS' ENTERED AT 12:24:49 ON 05 SEP 2006
D QUE L24
D QUE L27
L152 11 SEA ABB=ON (L24 OR L27) NOT (L18 OR L139)

FILE 'WPIX' ENTERED AT 12:24:50 ON 05 SEP 2006
D QUE L58
D QUE L59
L153 3 SEA ABB=ON (L58 OR L59) NOT (L39 OR L40 OR L31)

FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS, ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED AT 12:24:53 ON 05 SEP 2006
D QUE L79
L154 12 SEA ABB=ON L79 NOT (L75 OR L68)

FILE 'MEDLINE' ENTERED AT 12:25:02 ON 05 SEP 2006
D QUE L105
L155 10 SEA ABB=ON L105 NOT (L92 OR L83)

FILE 'EMBASE' ENTERED AT 12:25:03 ON 05 SEP 2006
D QUE L138
L156 1 SEA ABB=ON L138 NOT (L119 OR L110)

FILE 'STNGUIDE' ENTERED AT 12:25:10 ON 05 SEP 2006

FILE 'MEDLINE, CAPLUS, WPIX, EMBASE, DRUGU, PASCAL, BIOTECHNO, ESBIOBASE' ENTERED AT 12:25:33 ON 05 SEP 2006
L157 34 DUP REM L155 L152 L153 L156 L154 (3 DUPLICATES REMOVED)
ANSWERS '1-10' FROM FILE MEDLINE
ANSWERS '11-21' FROM FILE CAPLUS
ANSWERS '22-24' FROM FILE WPIX
ANSWER '25' FROM FILE EMBASE
ANSWERS '26-27' FROM FILE DRUGU
ANSWERS '28-29' FROM FILE BIOTECHNO
ANSWERS '30-34' FROM FILE ESBIOBASE
D IALL 1-10
D IBIB ED ABS HITIND 11-21
D IALL ABEQ TECH 22-24
D IALL 25-34

```
=> fil reg; d ide
FILE 'REGISTRY' ENTERED AT 09:59:23 ON 05 SEP 2006
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
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STRUCTURE FILE UPDATES:    4 SEP 2006  HIGHEST RN 905816-92-4
DICTIONARY FILE UPDATES:   4 SEP 2006  HIGHEST RN 905816-92-4

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TSCA INFORMATION NOW CURRENT THROUGH June 30, 2006

  Please note that search-term pricing does apply when
  conducting SmartSELECT searches.

REGISTRY includes numerically searchable data for experimental and
predicted properties as well as tags indicating availability of
experimental property data in the original document.  For information
on property searching in REGISTRY, refer to:

http://www.cas.org/ONLINE/UG/regprops.html



L11  ANSWER 1 OF 1  REGISTRY  COPYRIGHT 2006 ACS on STN
RN   372092-80-3  REGISTRY
ED   Entered STN:  28 Nov 2001
CN   Kinase (phosphorylating), protein (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   Neurokinase
CN   Protein kinase
MF   Unspecified
CI   MAN
SR   CA
LC   STN Files:   BIOSIS, CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
            1917 REFERENCES IN FILE CA (1907 TO DATE)
              17 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
            1930 REFERENCES IN FILE CAPLUS (1907 TO DATE)


=> =>
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=>
=> fil capl; d que l1; d que l6
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FILE LAST UPDATED: 4 Sep 2006  (20060904/ED)

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Inventor search

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L1             1 SEA FILE=CAPLUS ABB=ON  US99-235416/PRN


L2            45 SEA FILE=CAPLUS ABB=ON  SAKOWICZ R?/AU
L3          1091 SEA FILE=CAPLUS ABB=ON  GOLDSTEIN L?/AU
L4            61 SEA FILE=CAPLUS ABB=ON  (THERMOMYCES LANUGINOSUS/OBI OR
                 TL/OBI)(W)GAMMA/OBI
L6             9 SEA FILE=CAPLUS ABB=ON  (L2 AND L3) OR ((L2 OR L3) AND L4)


=> s l1 or l6

L139           9 L1 OR L6

=> fil wpix; d que l31

FILE 'WPIX' ENTERED AT 12:14:49 ON 05 SEP 2006
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FILE LAST UPDATED:          1 SEP 2006      <20060901/UP>
MOST RECENT DERWENT UPDATE:     200656        <200656/DW>
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L28 36 SEA FILE=WPIX ABB=ON SAKOWICZ R?/AU
L29 64 SEA FILE=WPIX ABB=ON GOLDSTEIN L?/AU
L31 3 SEA FILE=WPIX ABB=ON L28 AND L29

=> fil DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS,ESBIOBASE,
LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH

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=> d que l68

L61          138 SEA SAKOWICZ R?/AU
L62         4782 SEA GOLDSTEIN L?/AU
L63          147 SEA (THERMOMYCES LANUGINOSUS OR TL)(A) GAMMA
L68           40 SEA (L61 AND L62) OR ((L61 OR L62) AND L63)


=> fil medl; d que l83

FILE 'MEDLINE' ENTERED AT 12:14:52 ON 05 SEP 2006

 FILE LAST UPDATED: 2 Sep 2006 (20060902/UP). FILE COVERS 1950 TO DATE.

 On December 11, 2005, the 2006 MeSH terms were loaded.

 The MEDLINE reload for 2006 is now (26 Feb.) available. For details
 on the 2006 reload, enter HELP RLOAD at an arrow prompt (=>).
 See also:

    http://www.nlm.nih.gov/mesh/
    http://www.nlm.nih.gov/pubs/techbull/nd04/nd04_mesh.html
    http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_med_data_changes.html
    http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_2006_MeSH.html

 OLDMEDLINE is covered back to 1950.

 MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the
 MeSH 2006 vocabulary.

 This file contains CAS Registry Numbers for easy and accurate
 substance identification.


L80           13 SEA FILE=MEDLINE ABB=ON  SAKOWICZ R?/AU
L81         1168 SEA FILE=MEDLINE ABB=ON  GOLDSTEIN L?/AU
L82           11 SEA FILE=MEDLINE ABB=ON  (THERMOMYCES LANUGINOSUS OR TL)(A)GAMM
                 A
L83            4 SEA FILE=MEDLINE ABB=ON  (L80 AND L81) OR ((L80 OR L81) AND
                 L82)


=> fil embase; d que l110

FILE 'EMBASE' ENTERED AT 12:14:54 ON 05 SEP 2006
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 FILE COVERS 1974 TO 5 Sep 2006 (20060905/ED)

 EMBASE has been reloaded. Enter HELP RLOAD for details.

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 and biweekly.

 This file contains CAS Registry Numbers for easy and accurate
 substance identification.
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L107          13 SEA FILE=EMBASE ABB=ON  SAKOWICZ R?/AU
L108         922 SEA FILE=EMBASE ABB=ON  GOLDSTEIN L?/AU
L109          16 SEA FILE=EMBASE ABB=ON  (THERMOMYCES LANUGINOSUS OR TL)(A)GAMMA

L110           5 SEA FILE=EMBASE ABB=ON  (L107 AND L108) OR ((L107 OR L108) AND
                 L109)


=> dup rem l83,l139,l31,l110,l68
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PROCESSING COMPLETED FOR L83
PROCESSING COMPLETED FOR L139
PROCESSING COMPLETED FOR L31
PROCESSING COMPLETED FOR L110
PROCESSING COMPLETED FOR L68
L140          26 DUP REM L83 L139 L31 L110 L68 (35 DUPLICATES REMOVED)
                 ANSWERS '1-4' FROM FILE MEDLINE
                 ANSWERS '5-10' FROM FILE CAPLUS
                 ANSWERS '11-21' FROM FILE BIOSIS
                 ANSWER '22' FROM FILE LIFESCI
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ANSWERS '23-24' FROM FILE CONFSCI
ANSWERS '25-26' FROM FILE SCISEARCH

=> d ibib ed abs 1-26

L140 ANSWER 1 OF 26 MEDLINE on STN DUPLICATE 5
ACCESSION NUMBER: 2000095847 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10631986
TITLE: Cloning and expression of kinesins from the thermophilic fungus Thermomyces lanuginosus.
AUTHOR: **Sakowicz R**; Farlow S; **Goldstein L S**
CORPORATE SOURCE: Howard Hughes Medical Institute, Department of Cellular and Molecular Medicine, School of Medicine, University of California, San Diego, La Jolla 92093-0683, USA.
CONTRACT NUMBER: GM35252 (NIGMS)
SOURCE: Protein science : a publication of the Protein Society, (1999 Dec) Vol. 8, No. 12, pp. 2705-10.
Journal code: 9211750. ISSN: 0961-8368.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200002
ENTRY DATE: Entered STN: 29 Feb 2000
Last Updated on STN: 29 Feb 2000
Entered Medline: 14 Feb 2000
ED Entered STN: 29 Feb 2000
Last Updated on STN: 29 Feb 2000
Entered Medline: 14 Feb 2000
AB The motor domain regions of three novel members of the kinesin superfamily TLKIF1, TLKIFC, and TLBIMC were identified in a thermophilic fungus Thermomyces lanuginosus. Based on sequence similarity, they were classified as members of the known kinesin families Unc104/KIF1, KAR3, and BIMC. TLKIF1 was subsequently expressed in Escherichia coli. The expression level was high, and the protein was mostly soluble, easy to purify, and enzymatically active. TLKIF1 is a monomeric kinesin motor, which in a gliding motility assay displays a robust plus-directed microtubule movement up to 2 microm/s. The discovery of TLKIF1 also demonstrates that a family of kinesin motors not previously found in fungi may in fact be used in this group of organisms.

L140 ANSWER 2 OF 26 MEDLINE on STN DUPLICATE 7
ACCESSION NUMBER: 1998202613 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9535660
TITLE: A marine natural product inhibitor of kinesin motors.
AUTHOR: **Sakowicz R**; Berdelis M S; Ray K; Blackburn C L; Hopmann C; Faulkner D J; **Goldstein L S**
CORPORATE SOURCE: Department of Pharmacology, Division of Cellular and Molecular Medicine, Howard Hughes Medical Institute, University of California, San Diego, 9500 Gilman Drive, La Jolla, CA 92093-0683, USA.
SOURCE: Science, (1998 Apr 10) Vol. 280, No. 5361, pp. 292-5.
Journal code: 0404511. ISSN: 0036-8075.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199804
ENTRY DATE: Entered STN: 7 May 1998
Last Updated on STN: 7 May 1998

Entered Medline: 28 Apr 1998
ED Entered STN: 7 May 1998
Last Updated on STN: 7 May 1998
Entered Medline: 28 Apr 1998
AB Members of the kinesin superfamily of motor proteins are essential for mitotic and meiotic spindle organization, chromosome segregation, organelle and vesicle transport, and many other processes that require microtubule-based transport. A compound, adociasulfate-2, was isolated from a marine sponge, Haliclona (also known as Adocia) species, that inhibited kinesin activity by targeting its motor domain and mimicking the activity of the microtubule. Thus, the kinesin-microtubule interaction site could be a useful target for small molecule modulators, and adociasulfate-2 should serve as an archetype for specific inhibitors of kinesin functions.

L140 ANSWER 3 OF 26 MEDLINE on STN DUPLICATE 9
ACCESSION NUMBER: 1998028574 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9363944
TITLE: CENP-E is a plus end-directed kinetochore motor required for metaphase chromosome alignment.
AUTHOR: Wood K W; **Sakowicz R; Goldstein L S;** Cleveland D W
CORPORATE SOURCE: Laboratory of Cell Biology, Ludwig Institute for Cancer Research, University of California at San Diego, La Jolla 92093-0660, USA.
SOURCE: Cell, (1997 Oct 31) Vol. 91, No. 3, pp. 357-66.
Journal code: 0413066. ISSN: 0092-8674.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF027728
ENTRY MONTH: 199712
ENTRY DATE: Entered STN: 9 Jan 1998
Last Updated on STN: 9 Jan 1998
Entered Medline: 10 Dec 1997
ED Entered STN: 9 Jan 1998
Last Updated on STN: 9 Jan 1998
Entered Medline: 10 Dec 1997
AB Mitosis requires dynamic attachment of chromosomes to spindle microtubules. This interaction is mediated largely by kinetochores. During prometaphase, forces exerted at kinetochores, in combination with polar ejection forces, drive congression of chromosomes to the metaphase plate. A major question has been whether kinetochore-associated microtubule motors play an important role in congression. Using immunodepletion from and antibody addition to Xenopus egg extracts, we show that the kinetochore-associated kinesin-like motor protein CENP-E is essential for positioning chromosomes at the metaphase plate. We further demonstrate that CENP-E powers movement toward microtubule plus ends in vitro. These findings support a model in which CENP-E functions in congression to tether kinetochores to dynamic microtubule plus ends.

L140 ANSWER 4 OF 26 MEDLINE on STN
ACCESSION NUMBER: 96196874 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8612068
TITLE: The muscle in kinesin.
AUTHOR: **Sakowicz R; Goldstein L S**
SOURCE: Nature structural biology, (1996 May) Vol. 3, No. 5, pp. 404-7.
Journal code: 9421566. ISSN: 1072-8368.

PUB. COUNTRY: United States
DOCUMENT TYPE: News Announcement
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199606
ENTRY DATE: Entered STN: 13 Jun 1996
Last Updated on STN: 13 Jun 1996
Entered Medline: 3 Jun 1996
ED Entered STN: 13 Jun 1996
Last Updated on STN: 13 Jun 1996
Entered Medline: 3 Jun 1996

L140 ANSWER 5 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 1
ACCESSION NUMBER: 1999:487304 CAPLUS
DOCUMENT NUMBER: 131:112405
TITLE: Identification and expression of the microtubule motor protein kinesin **TL-γ**
INVENTOR(S): **Sakowicz, Roman; Goldstein, Lawrence S. B.**
PATENT ASSIGNEE(S): The Regents of the University of California, USA
SOURCE: PCT Int. Appl., 75 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE	
WO 9937659	A1	19990729	WO 1999-US1355		19990122	
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM						
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG						
AU 9924648	A1	19990809	AU 1999-24648		19990122	
US 6723840	B1	20040420	US 2000-724586		20001128	<--
US 6815169	B1	20041109	US 2000-724666		20001128	<--
US 6764830	B1	20040720	US 2000-600823		20001221	<--
PRIORITY APPLN. INFO.:			US 1998-72361P	A2	19980123	
			US 1999-235416	A3	19990122	<--
			WO 1999-US1355	W	19990122	

ED Entered STN: 06 Aug 1999
AB The invention concerns the isolation of a nucleic acid sequence from Thermomyces lanuginosus that encodes the microtubule motor protein kinesin TL-γ with the following properties: the protein's activity includes plus end-directed microtubule motor activity; the protein has a tail domain that has greater than 60% amino acid sequence identity to a TL-γ tail domain as measured using a sequence comparison algorithm; the protein specifically binds to polyclonal antibodies to TL-γ. The invention also concerns antibodies to TL-γ, methods for screening biol. active TL-γ, and kits for screening. Using PCR and degenerate primers, TL-γ was amplified from Thermomyces lanuginosus genomic DNA. The nucleic acid sequence was then used as a probe to isolate a longer TL-γ sequence. Recombinant TL-γ was prepared in order to test its activity in a microtubule gliding assay. The

pET23-TL-γ expression vector was constructed and expressed in E. coli. The kinesin TL-γ protein was isolated, it was very stable retaining 100% activity up to 40° after incubation for 15 min as measured using a microtubule dependent ATPase assay. Freshly prepared protein was used to assay microtubule gliding activity. Taxol stabilized microtubule seeds brightly labeled with rhodamine were prepared by incubating a 1:1 ratio of rhodamine labeled bovine brain tubulin; also unlabeled bovine brain tubulin was incorporated into the assay. Flow chambers prepared were preadsorbed with TL-γ motor protein. A microtubule/ATP mix containing polarity marked microtubules, taxol, MgATP and an oxygen scavenging system was then flowed into the chamber. Movement of microtubules was monitored at room temperature on a fluorescence microscope fitted with oil immersion objective and a CCD. For TL-γ activity measurement, recombinant TL-γ protein was attached to a glass coverslip using non-specific adhesion, and gliding of polarity marked microtubules containing brightly fluorescent rhodamine labeled seeds near their minus ends was recorded by time-lapse digital fluorescence microscopy. Microtubules moved with brightly fluorescent seeds leading, indicating that the immobilized TL-γ protein was moving toward microtubule plus ends. No movement was observed in the absence of TL-γ. This experiment demonstrates that TL-γ has plus-ended microtubule motor activity.

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L140 ANSWER 6 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 2
ACCESSION NUMBER: 1999:451195 CAPLUS
DOCUMENT NUMBER: 131:97592
TITLE: Kinesin motor modulators derived from the marine sponge adocia
INVENTOR(S): **Goldstein, Lawrence S. B.**; Faulkner, David John; **Sakowicz, Roman**; Berdelis, Michael S.; Blackburn, Christine L.; Hopmann, Cordula
PATENT ASSIGNEE(S): The Regents of the University of California, USA
SOURCE: PCT Int. Appl., 73 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9934806	A1	19990715	WO 1999-US321	19990106
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9921071	A1	19990726	AU 1999-21071	19990106
EP 1049475	A1	20001108	EP 1999-901353	19990106
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
US 6207403	B1	20010327	US 1999-226772	19990106
JP 2002500190	T2	20020108	JP 2000-527255	19990106
US 6489134	B1	20021203	US 2000-724609	20001128

US 2003127621	A1	20030710	US 2002-305857	20021127
US 6777200	B2	20040817		
US 2004176625	A1	20040909	US 2004-794757	20040303
PRIORITY APPLN. INFO.:			US 1998-70772P	P 19980108
			US 1999-226772	A3 19990106
			WO 1999-US321	W 19990106
			US 2000-724609	A1 20001128
			US 2002-305857	A1 20021127

OTHER SOURCE(S): MARPAT 131:97592
ED Entered STN: 23 Jul 1999
AB This invention provides novel compds. derived from a marine sponge, Adocia sp., that specifically modulate kinesin activity by targeting the kinesin motor domain and mimicking the activity of a microtubule. The compds. act as potent anti-mitogens and are useful in a wide variety of in vitro and in vivo applications [e.g. in mitigating a variety of pathol. conditions characterized by abnormal cell mitosis].
REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L140 ANSWER 7 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 3
ACCESSION NUMBER: 1999:194248 CAPLUS
DOCUMENT NUMBER: 130:233824
TITLE: Plus end-directed microtubule motor protein CENP-E required for Xenopus chromosome congression
INVENTOR(S): Wood, Kenneth W.; **Sakowicz, Roman**; **Goldstein, Lawrence S. B.**; Cleveland, Don W.
PATENT ASSIGNEE(S): The Regents of the University of California, USA
SOURCE: PCT Int. Appl., 78 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9913061	A1	19990318	WO 1998-US19231	19980910
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2303484	AA	19990318	CA 1998-2303484	19980910
AU 9893918	A1	19990329	AU 1998-93918	19980910
AU 745385	B2	20020321		
EP 1012249	A1	20000628	EP 1998-947039	19980910
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2001526881	T2	20011225	JP 2000-510850	19980910
US 6645748	B1	20031111	US 1998-150867	19980910
US 7009043	B1	20060307	US 2000-724584	20001128
US 2005191631	A1	20050901	US 2003-650280	20030827
PRIORITY APPLN. INFO.:			US 1997-58645P	P 19970911
			US 1998-150867	A1 19980910
			WO 1998-US19231	W 19980910

ED Entered STN: 25 Mar 1999
AB The invention provides isolated nucleic acid and amino acid sequences of

Xenopus centromere-associated protein-E (XCENP-E), antibodies to XCENP-E, methods of screening for CENP-E modulators using biol. active CENP-E, and kits for screening for CENP-E modulators. The full-length cDNA sequences of XCENP-E encodes a protein of 2954 amino acids with a predicted mol. mass of 340 kDa. XCENP-E is a member of the kinesin superfamily of motor proteins, and consists of a 500-amino acid globular N-terminal domain containing a kinesin-like microtubule motor domain linked to a globular tail domain by a region predicted to form a long, discontinuous α-helical coiled coil. The is the first biol. active CENP-E isolated and, surprisingly and contrary to previous reports, it demonstrates a motor that powers chromosome movement toward microtubule plus ends. Using immunodepletion and antibody addition to Xenopus egg exts., the present invention further demonstrates that CENP-E plays an essential role in congression.

REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L140 ANSWER 8 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 4
ACCESSION NUMBER: 1999:420033 CAPLUS
DOCUMENT NUMBER: 131:211782
TITLE: Adociasulfates 1-6, inhibitors of kinesin motor proteins from the sponge Haliclona (aka Adocia) sp.
AUTHOR(S): Blackburn, Christine L.; Hopmann, Cordula; **Sakowicz, Roman**; Berdelis, Michael S.; **Goldstein, Lawrence S. B.**; Faulkner, D. John
CORPORATE SOURCE: Scripps Institution of Oceanography, University of California at San Diego, La Jolla, CA, 92093-0212, USA
SOURCE: Journal of Organic Chemistry (1999), 64(15), 5565-5570
CODEN: JOCEAH; ISSN: 0022-3263
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 08 Jul 1999
GI

* STRUCTURE DIAGRAM TOO LARGE FOR DISPLAY - AVAILABLE VIA OFFLINE PRINT *

AB Adociasulfates 1-6 were isolated from an extract of the Palauan sponge Haliclona (aka Adocia) sp. that inhibited the transport of stabilized microtubules by the motor protein kinesin, which was immobilized on a microscope slide. The structures of adociasulfates 1-6, the relative stereochem. of adociasulfates 1 (I), 2, 5, and 6, and the relative stereochem. of subunits of adociasulfates 3 (II) and 4 were determined by interpretation of spectroscopic data. In a quant. assay that measures ATP hydrolysis by kinesin, adociasulfates 2 and 6 were the most active.

REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L140 ANSWER 9 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 10
ACCESSION NUMBER: 1996:282241 CAPLUS
DOCUMENT NUMBER: 124:310323
TITLE: The muscle in kinesin
AUTHOR(S): **Sakowicz, Roman; Goldstein, Lawrence S. B.**
CORPORATE SOURCE: Howard Hughes Medical Inst., Univ. California, La Jolla, CA, 92093-0683, USA
SOURCE: Nature Structural Biology (1996), 3(5), 404-407

Searched by Barb O'Bryen, STIC 2-2518

CODEN: NSBIEW; ISSN: 1072-8368
PUBLISHER: Nature Publishing Co.
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
ED Entered STN: 14 May 1996
AB A review, with 41 refs. The first high resolution structures of the kinesin and NCD motor proteins reveal their surprising similarity to myosin but leave open the tantalizing question of what properties eet. the directionality of movement along microtubules.

L140 ANSWER 10 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 11
ACCESSION NUMBER: 1997:151799 CAPLUS
DOCUMENT NUMBER: 126:234999
TITLE: Single molecules solvated in pores of polyacrylamide gels
AUTHOR(S): Dickson, Robert M.; Norris, D. J.; Tzeng, Yih-Ling; **Sakowicz, R.; Goldstein, L. S. B.**; Moerner, W. E.
CORPORATE SOURCE: Department Chemistry Biochemistry, University California San Diego, La Jolla, CA, 92093-0340, USA
SOURCE: Molecular Crystals and Liquid Crystals Science and Technology, Section A: Molecular Crystals and Liquid Crystals (1996), 291, 31-39
CODEN: MCLCE9; ISSN: 1058-725X
PUBLISHER: Gordon & Breach
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 08 Mar 1997
AB Individual fluorescent mols. and individual singly-labeled proteins have been observed in the water-filled pores of poly(acrylamide) gels with far-field microscopy. The mol. range of motion is dramatically reduced by the gel framework, thus allowing single mols. to be studied in an aqueous environment for long periods of time. For the small fluorophores, the gel restricts Brownian motion by approx. two orders of magnitude in each direction, thus greatly enhancing the mol.'s detectability. In contrast to dry polymeric hosts, the gel is composed primarily of water and the majority of mols. remain in solution, thus making these gels an ideal medium in which to utilize single mol. detection methods for the study of biol. systems in vitro.

L140 ANSWER 11 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN DUPLICATE 6
ACCESSION NUMBER: 1999:185585 BIOSIS
DOCUMENT NUMBER: PREV199900185585
TITLE: Single-molecule studies of fluorescent proteins and enzymes.
AUTHOR(S): Moerner, W. E. [Reprint author]; Peterman, E. J.; Sosa, H.; Brasselet, S.; Dickson, R. M.; Kummer, S.; **Sakowicz, R.; Goldstein, L. S. B.**
CORPORATE SOURCE: Department of Chemistry, Stanford University, Stanford, CA, USA
SOURCE: Biophysical Journal, (Jan., 1999) Vol. 76, No. 1 PART 2, pp. A20. print.
Meeting Info.: Forty-third Annual Meeting of the Biophysical Society. Baltimore, Maryland, USA. February 13-17, 1999.
CODEN: BIOJAU. ISSN: 0006-3495.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English

ENTRY DATE: Entered STN: 5 May 1999
Last Updated on STN: 5 May 1999
ED Entered STN: 5 May 1999
Last Updated on STN: 5 May 1999

L140 ANSWER 12 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN DUPLICATE 8
ACCESSION NUMBER: 1999:15470 BIOSIS
DOCUMENT NUMBER: PREV199900015470
TITLE: Study of the orientation of kinesin motors bound to microtubules using single molecule fluorescence polarization spectroscopy.
AUTHOR(S): Sosa, H. [Reprint author]; Peterman, E. J. G.; Dickson, R. M.; **Sakowicz, R.**; Moerner, W. E.; **Goldstein, L. G.**
CORPORATE SOURCE: Dep. Pharmacology, Univ. Calif., San Diego, CA 92093, USA
SOURCE: Molecular Biology of the Cell, (Nov., 1998) Vol. 9, No. SUPPL., pp. 28A. print.
Meeting Info.: 38th Annual Meeting of the American Society for Cell Biology. San Francisco, California, USA. December 12-16, 1998. American Society for Cell Biology.
CODEN: MBCEEV. ISSN: 1059-1524.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 20 Jan 1999
Last Updated on STN: 20 Jan 1999
ED Entered STN: 20 Jan 1999
Last Updated on STN: 20 Jan 1999

L140 ANSWER 13 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2006:342933 BIOSIS
DOCUMENT NUMBER: PREV200600349154
TITLE: Plus end-directed microtubule motor required for chromosome congression.
AUTHOR(S): Wood, Kenneth W. [Inventor]; **Sakowicz, Roman** [Inventor]; **Goldstein, Lawrence S. B.** [Inventor]; Cleveland, Don W. [Inventor]
CORPORATE SOURCE: Foster City, CA USA
ASSIGNEE: The Regents of the University of California
PATENT INFORMATION: US 07009043 20060307
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (MAR 7 2006)
CODEN: OGUPE7. ISSN: 0098-1133.
DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 12 Jul 2006
Last Updated on STN: 12 Jul 2006
ED Entered STN: 12 Jul 2006
Last Updated on STN: 12 Jul 2006
AB The invention provides isolated nucleic acid and amino acid sequences of Xenopus CENP-E (XCENP-E), antibodies to XCENP-E, methods of screening for CENP-E modulators using biologically active CENP-E, and kits for screening for CENP-E modulators.

L140 ANSWER 14 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2004:468880 BIOSIS
DOCUMENT NUMBER: PREV200400473914

TITLE: Identification and expression of a novel kinesin motor protein.
AUTHOR(S): **Sakowicz, Roman** [Inventor, Reprint Author]; **Goldstein, Lawrence S. B.** [Inventor]
CORPORATE SOURCE: ASSIGNEE: The Regents of the University of California
PATENT INFORMATION: US 6815169 20041109
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Nov 9 2004) Vol. 1288, No. 2. http://www.uspto.gov/web/menu/patdata.html. e-file. ISSN: 0098-1133 (ISSN print).
DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 9 Dec 2004
Last Updated on STN: 9 Dec 2004
ED Entered STN: 9 Dec 2004
Last Updated on STN: 9 Dec 2004
AB The invention provides isolated nucleic acid and amino acid sequences of **TL-gamma**, antibodies to **TL-gamma**, methods of screening for **TL-gamma** modulators using biologically active **TL-gamma**, and kits for screening for **TL-gamma** modulators.

L140 ANSWER 15 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN .
ACCESSION NUMBER: 2004:376082 BIOSIS
DOCUMENT NUMBER: PREV200400381987
TITLE: Kinesin motor modulators derived from the marine sponge Adocia.
AUTHOR(S): **Goldstein, Lawrence S. B.** [Inventor, Reprint Author]; Faulkner, David John [Inventor]; **Sakowicz, Roman** [Inventor]; Berdelis, Michael S. [Inventor]; Blackburn, Christine L. [Inventor]; Hopmann, Cordula [Inventor]
CORPORATE SOURCE: Frankfurt am Main, Germany
ASSIGNEE: The Regents of the University of California
PATENT INFORMATION: US 6777200 20040817
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Aug 17 2004) Vol. 1285, No. 3. http://www.uspto.gov/web/menu/patdata.html. e-file. ISSN: 0098-1133 (ISSN print).
DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 22 Sep 2004
Last Updated on STN: 22 Sep 2004
ED Entered STN: 22 Sep 2004
Last Updated on STN: 22 Sep 2004
AB This invention provides novel compounds derived from a marine sponge, Adocia sp., that specifically modulat kinesin activity by targeting the kinesin motor domain and mimicking the activity a microtubule. The compounds act as potent anti-mitogens are useful in a wide variety of in vitro and in vivo applications.

L140 ANSWER 16 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2004:332625 BIOSIS
DOCUMENT NUMBER: PREV200400337426
TITLE: Thermomyces lanuginosus kinesin motor protein and methods of screening for modulators of kinesin proteins.
AUTHOR(S): **Sakowicz, Roman** [Inventor, Reprint Author]; **Goldstein, Lawrence S. B.** [Inventor]

CORPORATE SOURCE: ASSIGNEE: The Regents of the University of California
PATENT INFORMATION: US 6764830 20040720
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (July 20 2004) Vol. 1284, No. 3. http://www.uspto.gov/web/menu/patdata.html. e-file. ISSN: 0098-1133 (ISSN print).
DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 4 Aug 2004
Last Updated on STN: 4 Aug 2004
ED Entered STN: 4 Aug 2004
Last Updated on STN: 4 Aug 2004
AB The invention provides isolated nucleic acid and amino acid sequences of **TL-gamma**, antibodies to **TL-gamma**, methods of screening for **TL-gamma** modulating using biologically active **TL-gamma**, and kits for screening for **TL-gamma** modulators.

L140 ANSWER 17 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2004:7637 BIOSIS
DOCUMENT NUMBER: PREV200400008401
TITLE: Plus end-directed microtubule motor required for chromosome congression.
AUTHOR(S): Wood, Kenneth W. [Inventor, Reprint Author]; **Sakowicz, Roman** [Inventor]; **Goldstein, Lawrence S. B.** [Inventor]; Cleveland, Don W. [Inventor]
CORPORATE SOURCE: Delmar, CA, USA
ASSIGNEE: The Regents of the University of California
PATENT INFORMATION: US 6645748 20031111
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Nov 11 2003) Vol. 1276, No. 2. http://www.uspto.gov/web/menu/patdata.html. e-file. ISSN: 0098-1133 (ISSN print).
DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 17 Dec 2003
Last Updated on STN: 17 Dec 2003
ED Entered STN: 17 Dec 2003
Last Updated on STN: 17 Dec 2003
AB The invention provides isolated nucleic acid and amino acid sequences of Xenopus CENP-E (XCENP-E), antibodies to XCENP-E, methods of screening for CENP-E modulators using biologically active CENP-E, and kits for screening for CENP-E modulators.

L140 ANSWER 18 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2003:56963 BIOSIS
DOCUMENT NUMBER: PREV200300056963
TITLE: Kinesin motor modulators derived from the marine sponge Adocia.
AUTHOR(S): **Goldstein, Lawrence S.B.** [Inventor, Reprint Author]; Faulkner, David John [Inventor]; **Sakowicz, Roman** [Inventor]; Berdelis, Michael S. [Inventor]; Blackburn, Christine L. [Inventor]; Hopmann, Cordula [Inventor]
CORPORATE SOURCE: San Diego, CA, USA
ASSIGNEE: The Regents of the University of California
PATENT INFORMATION: US 6489134 20021203
SOURCE: Official Gazette of the United States Patent and Trademark

Office Patents, (Dec 3 2002) Vol. 1265, No. 1.
http://www.uspto.gov/web/menu/patdata.html. e-file.
ISSN: 0098-1133 (ISSN print).
DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 22 Jan 2003
Last Updated on STN: 22 Jan 2003
ED Entered STN: 22 Jan 2003
Last Updated on STN: 22 Jan 2003
AB This invention provides novel compounds derived from a marine sponge, Adocia sp., that specifically modulat kinesin activity by targeting the kinesin motor domain and mimicking the activity a microtubule. The compounds act as potent anti-mitogens are useful in a wide variety of in vitro and in vivo applications.

L140 ANSWER 19 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2001:461909 BIOSIS
DOCUMENT NUMBER: PREV200100461909
TITLE: Kinesin motor modulators derived from the marine sponge Adocia.
AUTHOR(S): **Goldstein, Lawrence S. B.** [Inventor, Reprint author]; Faulkner, David John [Inventor]; **Sakowicz, Roman** [Inventor]; Berdelis, Michael S. [Inventor]; Blackburn, Christine L. [Inventor]; Hopmann, Cordula [Inventor]
CORPORATE SOURCE: San Diego, CA, USA
ASSIGNEE: The Regents of the University of California
PATENT INFORMATION: US 6207403 20010327
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Mar. 27, 2001) Vol. 1244, No. 4. e-file.
CODEN: OGUPE7. ISSN: 0098-1133.
DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 3 Oct 2001
Last Updated on STN: 22 Feb 2002
ED Entered STN: 3 Oct 2001
Last Updated on STN: 22 Feb 2002
AB This invention provides novel compounds derived from a marine sponge, Adocia sp., that specifically modulat kinesin activity by targeting the kinesin motor domain and mimicking the activity a microtubule. The compounds act as potent anti-mitogens are useful in a wide variety of in vitro and in vivo applications.

L140 ANSWER 20 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 1998:20152 BIOSIS
DOCUMENT NUMBER: PREV199800020152
TITLE: CENP-E is a plus end-directed kinetochore motor required for chromosome congression.
AUTHOR(S): Wood, K. W. [Reprint author]; **Sakowicz, R.**; **Goldstein, L. S. B.**; Cleveland, D. W. [Reprint author]
CORPORATE SOURCE: Lab. Cell Biol., Ludwig Inst. Cancer Research, La Jolla, CA 92093-0660, USA
SOURCE: Molecular Biology of the Cell, (Nov., 1997) Vol. 8, No. SUPPL., pp. 125A. print.
Meeting Info.: 37th Annual Meeting of the American Society for Cell Biology. Washington, D.C., USA. December 13-17, 1997. American Society for Cell Biology.

CODEN: MBCEEV. ISSN: 1059-1524.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 5 Jan 1998
Last Updated on STN: 5 Jan 1998
ED Entered STN: 5 Jan 1998
Last Updated on STN: 5 Jan 1998

L140 ANSWER 21 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 1997:95559 BIOSIS
DOCUMENT NUMBER: PREV199799394762
TITLE: Cloning, expression, and purification of kinesin superfamily members from the thermophilic fungus.
AUTHOR(S): **Sakowicz, R.**; Farlow, S.; **Goldstein, L. S. B.**
CORPORATE SOURCE: Howard Hughes Med. Inst., Div. Cell. Mol. Med., Dep. Pharmacol., Univ. Calif. San Diego, 9500 Gilman Dr., La Jolla, CA 92093-0683, USA
SOURCE: Molecular Biology of the Cell, (1996) Vol. 7, No. SUPPL., pp. 215A.
Meeting Info.: Annual Meeting of the 6th International Congress on Cell Biology and the 36th American Society for Cell Biology. San Francisco, California, USA. December 7-11, 1996.
CODEN: MBCEEV. ISSN: 1059-1524.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LANGUAGE: English
ENTRY DATE: Entered STN: 3 Mar 1997
Last Updated on STN: 3 Mar 1997
ED Entered STN: 3 Mar 1997
Last Updated on STN: 3 Mar 1997

L140 ANSWER 22 OF 26 LIFESCI COPYRIGHT 2006 CSA on STN
ACCESSION NUMBER: 2003:77194 LIFESCI
TITLE: Kinesin motor modulators derived from the marine sponge Adocia
AUTHOR: **Goldstein, L.S.B.**; Faulkner, D.J.; **Sakowicz, R.**; Berdelis, M.S.; Blackburn, C.L.; Hopmann, C.
CORPORATE SOURCE: The Regents of the University of California, Oakland, California
SOURCE: (20021203) . US Patent: 6489134; US CLASS: 435/21; 435/6; 514/172; 514/182; 514/518; 585/350.
DOCUMENT TYPE: Patent
FILE SEGMENT: Q4
LANGUAGE: English
SUMMARY LANGUAGE: English
AB This invention provides novel compounds derived from a marine sponge, Adocia sp., that specifically modulat kinesin activity by targeting the kinesin motor domain and mimicking the activity a microtubule. The compounds act as potent anti-mitogens are useful in a wide variety of in vitro and in vivo applications.

L140 ANSWER 23 OF 26 CONFSCI COPYRIGHT 2006 CSA on STN
ACCESSION NUMBER: 1999:35078 CONFSCI
DOCUMENT NUMBER: 99-047572
TITLE: Single-molecule studies of fluorescent proteins and

enzymes. Topic(s): 09A 01D
AUTHOR: Moerner, W.E.; Peterman, E.J.; Sosa, H.; Brasselet, S.; Dickson, R.M.; Kummer, S.; **Sakowicz, R.**; **Goldstein, L.S.B.**
CORPORATE SOURCE: Stanford Univ., USA
SOURCE: Biophysical Society, 9650 Rockville Pike, Bethesda, MD 20814, USA; phone: (301) 530-7114; fax: (301) 530-7133; email: society@biophysics.faseb.org; URL: www.biophysics.faseb.org, Abstracts available. Price $25..
Meeting Info.: 991 0048: 43rd Annual Meeting of the Biophysical Society (9910048). Baltimore, MD (USA). 13-17 Feb 1999. Biophysical Society.
DOCUMENT TYPE: Conference
FILE SEGMENT: DCCP
LANGUAGE: English

L140 ANSWER 24 OF 26 CONFSCI COPYRIGHT 2006 CSA on STN
ACCESSION NUMBER: 1999:26143 CONFSCI
DOCUMENT NUMBER: 99-038637
TITLE: Study of the orientation of kinesin motors bound to microtubules using single molecule fluorescence polarization spectroscopy
AUTHOR: Sosa, H.; Peterman, E.J.G.; Dickson, R.M.; **Sakowicz, R.**; Moerner, W.E.; **Goldstein, L.G.**
CORPORATE SOURCE: Dep. Pharmacol., Univ. California at San Diego, CA 92093, USA
SOURCE: American Society for Cell Biology, 9650 Rockville Pike, Bethesda, MD 20814, USA; phone: (301) 530-7153; fax: (301) 530-7139; email: ascbinfo@ascb.org; URL: www.ascb.org/ascb/, Abstracts available. Price $45. Paper No. 159.
Meeting Info.: 984 0478: 38th American Society for Cell Biology Annual Meeting (9840478). San Francisco, CA (USA). 12-16 Dec 1998. ASCB, Bio-Rad, Genentech, Jeol USA, Johnson & Johnson, Leica, Leadership Alliance, Mark-Rambar Family Foundation.
DOCUMENT TYPE: Conference
FILE SEGMENT: DCCP
LANGUAGE: English

L140 ANSWER 25 OF 26 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 1997:848661 SCISEARCH
THE GENUINE ARTICLE: YF096
TITLE: CENP-E is a plus end-directed kinetochore motor required for chromosome congression
AUTHOR: Wood K W (Reprint); **Sakowicz R**; **Goldstein L S B**; Cleveland D W
CORPORATE SOURCE: UNIV CALIF SAN DIEGO, CELL BIOL LAB, LUDWIG INST CANC RES, LA JOLLA, CA 92093; UNIV CALIF SAN DIEGO, HOWARD HUGHES MED INST, DIV CELLULAR & MOL MED, LA JOLLA, CA 92093
COUNTRY OF AUTHOR: USA
SOURCE: MOLECULAR BIOLOGY OF THE CELL, (NOV 1997) Vol. 8, Supp. [S], pp. 723-723.
ISSN: 1059-1524.
PUBLISHER: AMER SOC CELL BIOLOGY, 8120 WOODMONT AVE, STE 750, BETHESDA, MD 20814-2755 USA.
DOCUMENT TYPE: Conference; Journal
LANGUAGE: English
REFERENCE COUNT: 0

ENTRY DATE: Entered STN: 1997
Last Updated on STN: 1997
ED Entered STN: 1997
Last Updated on STN: 1997

L140 ANSWER 26 OF 26 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 1997:46229 SCISEARCH
THE GENUINE ARTICLE: WB018
TITLE: Cloning, expression, and purification of kinesin superfamily members from the thermophilic fungus.
AUTHOR: **Sakowicz R (Reprint)**; Farlow S; **Goldstein L S B**
CORPORATE SOURCE: UNIV CALIF SAN DIEGO, DEPT PHARMACOL, DIV CELLULAR & MOL MED, HOWARD HUGHES MED INST, LA JOLLA, CA 92093
COUNTRY OF AUTHOR: USA
SOURCE: MOLECULAR BIOLOGY OF THE CELL, (DEC 1996) Vol. 7, Supp. [S], pp. 1250-1250.
ISSN: 1059-1524.
PUBLISHER: AMER SOC CELL BIOLOGY, 8120 WOODMONT AVE, STE 750, BETHESDA, MD 20814-2755 USA.
DOCUMENT TYPE: Conference; Journal
LANGUAGE: English
REFERENCE COUNT: 0
ENTRY DATE: Entered STN: 1997
Last Updated on STN: 1997
ED Entered STN: 1997
Last Updated on STN: 1997

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L9         20619 SEA FILE=CAPLUS ABB=ON  MICROTUBULE#/OBI
L10         3352 SEA FILE=CAPLUS ABB=ON  MOTOR/OBI(L)PROTEIN#/OBI
L11            1 SEA FILE=REGISTRY ABB=ON  "PROTEIN KINASE"/CN
L12        97768 SEA FILE=CAPLUS ABB=ON  L11 OR PROTEIN KINASE#/OBI
L14            1 SEA FILE=CAPLUS ABB=ON  L4 AND (L5 OR L7 OR L9 OR L10 OR L12)


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L30 1 SEA FILE=WPIX ABB=ON (THERMOMYCES LANUGINOSUS/BI,ABEX OR
TL/BI,ABEX)(A)GAMMA/BI,ABEX

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L144 0 L30 NOT L31 previously printed

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LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH

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FILE 'SCISEARCH' ENTERED AT 12:19:04 ON 05 SEP 2006

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L63 147 SEA (THERMOMYCES LANUGINOSUS OR TL)(A) GAMMA
L64 13861 SEA KINESIN#
L65 132140 SEA MICROTUBULE# OR MICRO TUBULE#
L66 7756 SEA MOTOR PROTEIN#
L67 2654 SEA END DIRECT?
L70 567385 SEA PROTEIN KINASE#
L71 3 SEA L63 AND (L64 OR L65 OR L66 OR L67 OR L70)

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L145 0 L71 NOT L68 previously printed

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FILE 'MEDLINE' ENTERED AT 12:19:12 ON 05 SEP 2006

FILE LAST UPDATED: 2 Sep 2006 (20060902/UP). FILE COVERS 1950 TO DATE.

On December 11, 2005, the 2006 MeSH terms were loaded.

The MEDLINE reload for 2006 is now (26 Feb.) available. For details on the 2006 reload, enter HELP RLOAD at an arrow prompt (=>). See also:

http://www.nlm.nih.gov/mesh/
http://www.nlm.nih.gov/pubs/techbull/nd04/nd04_mesh.html
http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_med_data_changes.html
http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_2006_MeSH.html

OLDMEDLINE is covered back to 1950.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2006 vocabulary.

This file contains CAS Registry Numbers for easy and accurate substance identification.

L82 11 SEA FILE=MEDLINE ABB=ON (THERMOMYCES LANUGINOSUS OR TL)(A)GAMMA
L84 2094 SEA FILE=MEDLINE ABB=ON KINESIN/CT
L85 17967 SEA FILE=MEDLINE ABB=ON MICROTUBULES/CT
L86 76212 SEA FILE=MEDLINE ABB=ON ENZYME INHIBITORS/CT
L87 1529 SEA FILE=MEDLINE ABB=ON MOTOR PROTEIN#
L88 359 SEA FILE=MEDLINE ABB=ON END DIRECT?
L89 0 SEA FILE=MEDLINE ABB=ON L82 AND (L84 OR L85 OR L86 OR L87 OR L88)

```
=> fil embase; d que l118

FILE 'EMBASE' ENTERED AT 12:19:14 ON 05 SEP 2006
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 FILE COVERS 1974 TO 5 Sep 2006 (20060905/ED)

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 EMBASE is now updated daily.  SDI frequency remains weekly (default)
 and biweekly.

 This file contains CAS Registry Numbers for easy and accurate
 substance identification.


L109          16 SEA FILE=EMBASE ABB=ON  (THERMOMYCES LANUGINOSUS OR TL)(A)GAMMA

L112        2142 SEA FILE=EMBASE ABB=ON  KINESIN/CT
L113        3476 SEA FILE=EMBASE ABB=ON  MICROTUBULE ASSEMBLY/CT
L114         754 SEA FILE=EMBASE ABB=ON  MICROTUBULE PROTEIN/CT
L115       13611 SEA FILE=EMBASE ABB=ON  MICROTUBULE/CT
L116         316 SEA FILE=EMBASE ABB=ON  END DIRECT?
L117         569 SEA FILE=EMBASE ABB=ON  MOTOR PROTEIN/CT OR MOLECULAR MOTOR/CT

L118           0 SEA FILE=EMBASE ABB=ON  L109 AND (L112 OR L113 OR L114 OR L115
                 OR L116 OR L117)
```

```
=>
=> => fil capl; d que l18
FILE 'CAPLUS' ENTERED AT 12:20:57 ON 05 SEP 2006
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```
FILE COVERS 1907 - 5 Sep 2006  VOL 145 ISS 11
FILE LAST UPDATED: 4 Sep 2006  (20060904/ED)

Effective October 17, 2005, revised CAS Information Use Policies apply.
They are available for your review at:

http://www.cas.org/infopolicy.html
'OBI' IS DEFAULT SEARCH FIELD FOR 'CAPLUS' FILE


L7          1841 SEA FILE=CAPLUS ABB=ON  KINESINS/CT
L9         20619 SEA FILE=CAPLUS ABB=ON  MICROTUBULE#/OBI
L10         3352 SEA FILE=CAPLUS ABB=ON  MOTOR/OBI(L)PROTEIN#/OBI
L15          220 SEA FILE=CAPLUS ABB=ON  L7 AND L9 AND L10
L17           48 SEA FILE=CAPLUS ABB=ON  END DIRECT?/OBI
L18            3 SEA FILE=CAPLUS ABB=ON  L15 AND L17


=> s l18 not l139

L146           3 L18 NOT L139
```

previously printed

```
=> fil wpix; d que l39; d que l40

FILE 'WPIX' ENTERED AT 12:20:58 ON 05 SEP 2006
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FILE LAST UPDATED:          1 SEP 2006      <20060901/UP>
MOST RECENT DERWENT UPDATE:     200656        <200656/DW>
DERWENT WORLD PATENTS INDEX SUBSCRIBER FILE, COVERS 1963 TO DATE

>>> FOR A COPY OF THE DERWENT WORLD PATENTS INDEX STN USER GUIDE,
    PLEASE VISIT:
 http://www.stn-international.de/training_center/patents/stn_guide.pdf <

>>> FOR DETAILS OF THE PATENTS COVERED IN CURRENT UPDATES, SEE
http://scientific.thomson.com/support/patents/coverage/latestupdates/

>>> PLEASE BE AWARE OF THE NEW IPC REFORM IN 2006, SEE
http://www.stn-international.de/stndatabases/details/ipc_reform.html and
http://scientific.thomson.com/media/scpdf/ipcrdwpi.pdf <<<
```

```
>>> FOR FURTHER DETAILS ON THE FORTHCOMING DERWENT WORLD PATENTS
    INDEX ENHANCEMENTS PLEASE VISIT:
http://www.stn-international.de/stndatabases/details/dwpi_r.html <<<
'BI ABEX' IS DEFAULT SEARCH FIELD FOR 'WPIX' FILE


L32          252 SEA FILE=WPIX ABB=ON  KINESIN#/BI,ABEX
L33          811 SEA FILE=WPIX ABB=ON  MICROTUBULE#/BI,ABEX OR MICRO TUBULE#/BI,
                 ABEX
L34          120 SEA FILE=WPIX ABB=ON  MOTOR PROTEIN#/BI,ABEX
L35         1863 SEA FILE=WPIX ABB=ON  END DIRECT?/BI,ABEX
L39            3 SEA FILE=WPIX ABB=ON  L32 AND L33 AND L34 AND L35



L32          252 SEA FILE=WPIX ABB=ON  KINESIN#/BI,ABEX
L33          811 SEA FILE=WPIX ABB=ON  MICROTUBULE#/BI,ABEX OR MICRO TUBULE#/BI,
                 ABEX
L34          120 SEA FILE=WPIX ABB=ON  MOTOR PROTEIN#/BI,ABEX
L35         1863 SEA FILE=WPIX ABB=ON  END DIRECT?/BI,ABEX
L36         4006 SEA FILE=WPIX ABB=ON  PROTEIN KINASE#/BI,ABEX
L37          105 SEA FILE=WPIX ABB=ON  L32 AND (L33 OR L34 OR L35)
L40            1 SEA FILE=WPIX ABB=ON  L37 AND L36


=> s l39,l40 not l31

L147           3 (L39 OR L40) NOT (L31)  previously printed

=> fil DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS,ESBIOBASE,
LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH

FILE 'DRUGU' ENTERED AT 12:21:01 ON 05 SEP 2006
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FILE 'LIFESCI' ENTERED AT 12:21:01 ON 05 SEP 2006
```

FILE 'CONFSCI' ENTERED AT 12:21:01 ON 05 SEP 2006

FILE 'DISSABS' ENTERED AT 12:21:01 ON 05 SEP 2006

FILE 'JAPIO' ENTERED AT 12:21:01 ON 05 SEP 2006

FILE 'ANABSTR' ENTERED AT 12:21:01 ON 05 SEP 2006

FILE 'SCISEARCH' ENTERED AT 12:21:01 ON 05 SEP 2006


```
=> d que l75

L64        13861 SEA KINESIN#
L65       132140 SEA MICROTUBULE# OR MICRO TUBULE#
L66         7756 SEA MOTOR PROTEIN#
L67         2654 SEA END DIRECT?
L75           20 SEA L64 (5A) L65 (5A) L66 (5A) L67


=> s l75 not l68

L148          20 L75 NOT L68
```

previously printed

```
=> fil medl; d que l92

FILE 'MEDLINE' ENTERED AT 12:21:10 ON 05 SEP 2006

 FILE LAST UPDATED: 2 Sep 2006 (20060902/UP).  FILE COVERS 1950 TO DATE.

 On December 11, 2005, the 2006 MeSH terms were loaded.

 The MEDLINE reload for 2006 is now (26 Feb.) available.  For details
 on the 2006 reload, enter HELP RLOAD at an arrow prompt (=>).
 See also:

    http://www.nlm.nih.gov/mesh/
    http://www.nlm.nih.gov/pubs/techbull/nd04/nd04_mesh.html
    http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_med_data_changes.html
    http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_2006_MeSH.html

 OLDMEDLINE is covered back to 1950.

 MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the
 MeSH 2006 vocabulary.

 This file contains CAS Registry Numbers for easy and accurate
 substance identification.


L84         2094 SEA FILE=MEDLINE ABB=ON  KINESIN/CT
L85        17967 SEA FILE=MEDLINE ABB=ON  MICROTUBULES/CT
L87         1529 SEA FILE=MEDLINE ABB=ON  MOTOR PROTEIN#
```

```
L88          359 SEA FILE=MEDLINE ABB=ON  END DIRECT?
L92            9 SEA FILE=MEDLINE ABB=ON  L87(8A)L88 AND L84 AND L85


=> s l92 not l83

L149           9 L92 NOT L83
```

previously printed

```
=> fil embase; d que l119

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 This file contains CAS Registry Numbers for easy and accurate
 substance identification.


L112        2142 SEA FILE=EMBASE ABB=ON  KINESIN/CT
L113        3476 SEA FILE=EMBASE ABB=ON  MICROTUBULE ASSEMBLY/CT
L114         754 SEA FILE=EMBASE ABB=ON  MICROTUBULE PROTEIN/CT
L115       13611 SEA FILE=EMBASE ABB=ON  MICROTUBULE/CT
L116         316 SEA FILE=EMBASE ABB=ON  END DIRECT?
L117         569 SEA FILE=EMBASE ABB=ON  MOTOR PROTEIN/CT OR MOLECULAR MOTOR/CT

L119           7 SEA FILE=EMBASE ABB=ON  L112 AND (L113 OR L114 OR L115) AND
                 L116 AND L117


=> s l119 not l110

L150           7 L119 NOT L110
```

previously printed

```
=> => dup rem l149,l146,l147,l150,l148
FILE 'MEDLINE' ENTERED AT 12:21:44 ON 05 SEP 2006

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FILE 'LIFESCI' ENTERED AT 12:21:44 ON 05 SEP 2006

FILE 'SCISEARCH' ENTERED AT 12:21:44 ON 05 SEP 2006

PROCESSING COMPLETED FOR L149
PROCESSING COMPLETED FOR L146
PROCESSING COMPLETED FOR L147
PROCESSING COMPLETED FOR L150
PROCESSING COMPLETED FOR L148
L151 28 DUP REM L149 L146 L147 L150 L148 (14 DUPLICATES REMOVED)
ANSWERS '1-9' FROM FILE MEDLINE
ANSWERS '10-12' FROM FILE CAPLUS
ANSWERS '13-15' FROM FILE WPIX
ANSWERS '16-21' FROM FILE EMBASE
ANSWERS '22-23' FROM FILE BIOTECHNO
ANSWERS '24-27' FROM FILE BIOSIS
ANSWER '28' FROM FILE LIFESCI

=> d iall 1-9; d ibib ed abs hitind 10-12; d iall abeq tech 13-15; d iall 16-28

L151 ANSWER 1 OF 28 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2005237850 MEDLINE
DOCUMENT NUMBER: PubMed ID: 15875026
TITLE: The bipolar mitotic kinesin Eg5 moves on both microtubules that it crosslinks.
AUTHOR: Kapitein Lukas C; Peterman Erwin J G; Kwok Benjamin H; Kim Jeffrey H; Kapoor Tarun M; Schmidt Christoph F
CORPORATE SOURCE: Department of Physics and Astronomy and Laser Centre, Vrije Universiteit, De Boelelaan 1081, 1081 HV Amsterdam, The Netherlands.
SOURCE: Nature, (2005 May 5) Vol. 435, No. 7038, pp. 114-8.
Journal code: 0410462. E-ISSN: 1476-4687.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200505
ENTRY DATE: Entered STN: 6 May 2005
Last Updated on STN: 19 May 2005
Entered Medline: 18 May 2005
ABSTRACT:
During cell division, mitotic spindles are assembled by microtubule-based motor proteins. The bipolar organization of spindles is essential for proper segregation of chromosomes, and requires plus-**end-directed** homotetrameric **motor proteins** of the widely conserved kinesin-5 (BimC) family. Hypotheses for bipolar spindle formation include the 'push-pull mitotic muscle' model, in which kinesin-5 and opposing motor proteins act between overlapping microtubules. However, the precise roles of kinesin-5 during this process are unknown. Here we show that the vertebrate kinesin-5 Eg5 drives the sliding of microtubules depending on their relative orientation. We found in controlled in vitro assays that Eg5 has the remarkable capability of simultaneously moving at approximately 20 nm s(-1) towards the plus-ends of each of the two microtubules it crosslinks. For anti-parallel microtubules, this results in relative sliding at approximately 40 nm s(-1), comparable to spindle pole separation rates in vivo. Furthermore, we found that Eg5 can tether microtubule plus-ends, suggesting an additional

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: September 1, 2006, 14:22:02 ; Search time 187.583 Seconds
(without alignments)
1910.930 Million cell updates/sec

Title: US-09-235-416-1
Perfect score: 4030
Sequence: 1 MSGGGNIKVVVRVRPFNARE.....ELRQQQAQMEEALKTAKQEF 784

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4030	100.0	784	2	AAY06618	Aay06618 Thermomyc
2	1684.5	41.8	1714	8	ABM83648	Abm83648 Human dia
3	1684.5	41.8	1721	8	ABM83647	Abm83647 Human dia
4	1679	41.7	1199	8	ABM83671	Abm83671 Human dia
5	1674.5	41.6	1696	8	ABM83653	Abm83653 Human dia
6	1674.5	41.6	1709	8	ABM83649	Abm83649 Human dia
7	1674.5	41.6	1722	8	ABM83646	Abm83646 Human dia
8	1673	41.5	1708	8	ABM83650	Abm83650 Human dia
9	1669.5	41.4	1699	8	ABM83651	Abm83651 Human dia
10	1668.5	41.4	1816	3	AAB36227	Aab36227 Human kin
11	1667.5	41.4	1805	7	ADJ95088	Adj95088 Novel NOV
12	1666.5	41.4	1770	6	AAE35317	Aae35317 Mouse KIF
13	1661.5	41.2	1823	5	ABB07867	Abb07867 Human kin
14	1660.5	41.2	893	4	AAM40034	Aam40034 Human pol
15	1659.5	41.2	1697	8	ABM83652	Abm83652 Human dia
16	1658	41.1	1103	3	AAY51328	Aay51328 Human KLI
17	1658	41.1	1103	4	AAE04316	Aae04316 Human kin
18	1658	41.1	1103	6	ABG72054	Abg72054 Human kin
19	1658	41.1	1103	7	ADG63388	Adg63388 Human kin
20	1635	40.6	1773	4	ABB63908	Abb63908 Drosophil
21	1463.5	36.3	1805	5	ABP68930	Abp68930 Human pol
22	1431.5	35.5	1362	5	AAU74840	Aau74840 Human HsK
23	1430	35.5	757	4	AAU19569	Aau19569 Human dia
24	1430	35.5	757	5	ABP51294	Abp51294 Human MDD
25	1423	35.3	762	5	ABG60124	Abg60124 Human DIT
26	1413	35.1	1507	8	ADQ97525	Adq97525 Human can
27	1412	35.0	1826	7	ADJ69671	Adj69671 Human hea
28	1412	35.0	1826	8	ADL83235	Adl83235 Human PRO
29	1407.5	34.9	1844	8	ADQ97522	Adq97522 Mouse can
30	1396.5	34.7	1921	4	ABB62962	Abb62962 Drosophil
31	1386	34.4	1815	8	ADR66952	Adr66952 Human pro
32	1386	34.4	1815	8	ADR66054	Adr66054 Human pro
33	1386	34.4	1815	8	ADR66951	Adr66951 Human pro
34	1386	34.4	1815	8	ADR66053	Adr66053 Human pro
35	1347	33.4	944	7	ADM04401	Adm04401 Human pro
36	1347	33.4	944	9	AEC87331	Aec87331 Human cDN
37	1347	33.4	1317	9	AED07567	Aed07567 Chromosom
38	1347	33.4	1392	6	AAE32129	Aae32129 Human cyt
39	1347	33.4	1392	7	ADJ94858	Adj94858 Novel NOV
40	1347	33.4	1393	8	ADN00367	Adn00367 Novel hum
41	1311.5	32.5	1375	5	ABB79531	Abb79531 Human kin
42	1311.5	32.5	1375	5	ABB84481	Abb84481 Human HsK
43	1311.5	32.5	1375	5	AAE22525	Aae22525 Human HsK
44	1307	32.4	1394	7	ADJ94856	Adj94856 Novel NOV
45	1278.5	31.7	504	3	AAB63189	Aab63189 Gene 5 hu

ALIGNMENTS

RESULT 1
AAY06618
ID AAY06618 standard; protein; 784 AA.
XX
AC AAY06618;
XX
DT 26-OCT-1999 (first entry)
XX
DE Thermomyces lanuginosus kinesin motor protein TL-gamma.
XX
KW TL-gamma; kinesin; motor protein; microtubule; unc-104; infection;
KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; amyotrophic lateral sclerosis.
XX
OS Thermomyces lanuginosus.
XX
PN WO9937659-A1.
XX
PD 29-JUL-1999.
XX
PF 22-JAN-1999; 99WO-US001355.
XX
PR 23-JAN-1998; 98US-0072361P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Sakowicz R, Goldstein LSB;
XX
DR WPI; 1999-493950/41.
DR N-PSDB; AAX87656.
XX
PT New nucleic acid encoding microtubule motor protein, used for diagnosis
PT of fungal infection and neurodegenerative disease.
XX
PS Claim 5; Page 70-71; 75pp; English.
XX
CC This sequence represents Thermomyces lanuginosus TL-gamma, a novel ATP-
CC dependent, plus end-directed microtubule motor protein that is a member
CC of the unc-104 family and kinesin superfamily. The invention provides TL-
CC gamma nucleic acids (see AAX87656), proteins and antibodies, and methods
CC of screening for TL-gamma modulators potentially useful for treating
CC hyphal fungal infections and diseases caused by mutated TL-gamma, e.g.
CC neurodegeneration involving anterograde axonal transport, such as
CC Alzheimer's, Parkinson's or Huntington's diseases or amyotrophic lateral
CC sclerosis. Detection of TL-gamma allows differentiation between hyphal
CC and non-hyphal fungal infections

```
XX
SQ   Sequence 784 AA;

  Query Match             100.0%;  Score 4030;  DB 2;  Length 784;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-299;
  Matches  784;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSGGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSGGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPK 60

Qy         61 AFAFDRSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AFAFDRSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120

Qy        121 YGKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YGKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180

Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240

Qy        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS 300

Qy        301 GKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKRIK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKRIK 360

Qy        361 NHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGAGGSGGPVEESYPPDTPLEKQIV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGAGGSGGPVEESYPPDTPLEKQIV 420

Qy        421 SIQQPDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISI 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SIQQPDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISI 480

Qy        481 EKGFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKILK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EKGFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKILK 540

Qy        541 EHCTFENVDNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHPEEARAE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 EHCTFENVDNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHPEEARAE 600

Qy        601 RQEQSLLRHSVTNSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHFRGKDSDWFYARR 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RQEQSLLRHSVTNSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHFRGKDSDWFYARR 660

Qy        661 EAASAILGLDQKISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDSQSSFPVRDKYMSN 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 EAASAILGLDQKISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDSQSSFPVRDKYMSN 720

Qy        721 GTIDNFSLDTAITMPGTPRSDDDGDALFFGDKKSKQDASNVDVEELRQQQAQMEEALKTA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTIDNFSLDTAITMPGTPRSDDDGDALFFGDKKSKQDASNVDVEELRQQQAQMEEALKTA 780

Qy        781 KQEF 784
              ||||
Db        781 KQEF 784


RESULT 2
ABM83648
ID   ABM83648 standard; protein; 1714 AA.
XX
AC   ABM83648;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:3897.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS   Homo sapiens.
XX
PN   WO2004023973-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Schmidt JP,  Wright RJ,  Bruns CM,  Marjanovic MM,  Shen F;
PI   Harthshorne TA,  Suchorolski MT,  Altus CM,  Pitts SJ,  Elder LV;
PI   Mooney EM,  Delegeane AM,  Panesar IS,  Banville SC,  Reddy TP;
PI   Stevens KA,  Blanchard JL,  Panzer SR,  Wang X,  Au AP,  Gerstin EH;
PI   Peralta CH,  Anderson SB,  Rioux P,  Shen EJ,  Wu MC,  Stuve LL;
PI   Lagace RE,  Spiro PA,  Stewart EA,  Wingrove J,  Vitt UA,  Kirton ES;
PI   Xu Y,  Kwong M,  Policky JL,  Hurwitz BL,  Ma Y,  Jackson JL,  Gietzen D;
PI   Patury S,  Shi X,  Suarez CJ;
XX
DR   WPI; 2004-329368/30.
DR   N-PSDB; ACN42300.
XX
PT   New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT   in gene mapping.
XX
PS   Claim 27; Page; 190pp; English.
XX
CC   The invention relates to novel diagnostic and therapeutic polynucleotides
CC   selected from one of the 2722 sequences defined in the specification. A
CC   polynucleotide of the invention may have a use in gene therapy. The human
CC   diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC   used to diagnose a particular condition, disease or disorder associated
CC   with human molecules, e.g. cell proliferative disorders,
CC   autoimmune/inflammatory disorder, developmental disorder, endocrine
CC   disorder, neurological disorders, gastrointestinal disorders, or
CC   infections caused by virus, bacteria, fungi or parasite. The dithp
CC   molecules may also be used in genetic mapping, in identifying individuals
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp protein of the
CC   invention. Note: The sequence data for this patent is not represented in
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 1714 AA;

  Query Match             41.8%;  Score 1684.5;  DB 8;  Length 1714;
  Best Local Similarity   46.5%;  Pred. No. 6.4e-119;
  Matches  358;  Conservative  127;  Mismatches  174;  Indels  111;  Gaps   16;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||: | :|||::| |: | :  |   :|           ||:|:
Db          3 GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET----------PKSFS 51

Qy         64 FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
              || ||||    :|   ||| |: :::|:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG 109

Qy        121 YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
                 :  : |:||::|:|:| |||:   | |:: :|||||:||| |||||||||  ||||:|
Db        110 KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV 168

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
              ||||  |||||||:|| | |: :|::||| ||||||||||||||||||||||| :  |||
Db        169 REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK 228
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Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
Db        229 RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM 288

Qy        299 SSG-----KQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYA 353
Db        289 DSGPNKNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYA 348

Qy        354 DSAKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGG--------GGAG------ 399
Db        349 DRAKQIRCNAVINEDPNNKLIRELKDEVTRLRDLLYAQGLGDITDTNTVPGGPKYVSDLE 408

Qy        400 ----GSGGPVEESYPPDTPLEKQIVSIQQPDATVKKMS-----------------KAEI 437
Db        409 NNNLNRGGTVNEAPDPLSTVTNALVGM-SPSSSLSALSSRAASVSSLHERILFAPGSEEA 467

Qy        438 VEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISIEK--GFVGPYHSKEMPH 495
Db        468 IERLKETEKIIAELNETWEEKLRRTEAIRMEREALLAEMGVAMREDGGTLGVFSPKKTPH 527

Qy        496 LVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKILKEHCTFEN-----VDN 550
Db        528 LVNLNEDPLMSECLLYYIKDGITRVGREDGERRQDIVLSGHFIKEEHCVFRSDSRGGSEA 587

Qy        551 VVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHPEEARAERQEQSLLRHS 610
Db        588 VVTLEPCEGADTYVNGKKVTEPSILRSGNRIIMGKSHVFRFNHPEQARQERER------- 640

Qy        611 VTNSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHFRGKDSDWFYARREAASAILGLD 670
Db        641 -------------------------------TPCAETPAEPVDWAFAQRELLEK-QGID 667

Qy        671 QKISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDSQSSFPVRDKYMSN 720
Db        668 MK--QEMEQRLQELEDQYRREREEATYLLE-QQRLDYESKLEALQKQMDS 714
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RESULT 3
ABM83647
ID ABM83647 standard; protein; 1721 AA.
XX
AC ABM83647;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3896.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI; 2004-329368/30.
DR N-PSDB; ACN42299.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 1721 AA;

Query Match 41.8%; Score 1684.5; DB 8; Length 1721;
Best Local Similarity 46.5%; Pred. No. 6.5e-119;
Matches 358; Conservative 127; Mismatches 174; Indels 111; Gaps 16;

```
Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
Db          3 GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET-----------PKSFS 51

Qy         64 FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
Db         52 FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG 109

Qy        121 YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
Db        110 KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV 168

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
Db        169 REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK 228

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
Db        229 RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM 288

Qy        299 SSG-----KQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYA 353
Db        289 DSGPNKNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYA 348

Qy        354 DSAKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGG--------GGAG------ 399
Db        349 DRAKQIRCNAVINEDPNNKLIRELKDEVTRLRDLLYAQGLGDITDTNTVPGGPKYVSDLE 408

Qy        400 ----GSGGPVEESYPPDTPLEKQIVSIQQPDATVKKMS-----------------KAEI 437
Db        409 NNNLNRGGTVNEAPDPLSTVTNALVGM-SPSSSLSALSSRAASVSSLHERILFAPGSEEA 467

Qy        438 VEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISIEK--GFVGPYHSKEMPH 495
Db        468 IERLKETEKIIAELNETWEEKLRRTEAIRMEREALLAEMGVAMREDGGTLGVFSPKKTPH 527

Qy        496 LVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKILKEHCTFEN-----VDN 550
Db        528 LVNLNEDPLMSECLLYYIKDGITRVGREDGERRQDIVLSGHFIKEEHCVFRSDSRGGSEA 587

Qy        551 VVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHPEEARAERQEQSLLRHS 610
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Db        588 VVTLEPCEGADTYVNGKKVTEPSILRSGNRIIMGKSHVFRFNHPEQARQERER------- 640

Qy        611 VTNSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHFRGKDSDWFYARREAASAILGLD 670

Db        641 --------------------------------TPCAETPAEPVDWAFAQRELLEK-QGID 667

Qy        671 QKISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDSQSSFPVRDKYMSN 720

Db        668 MK--QEMEQRLQELEDQYRRREREEATYLLE-QQRLDYESKLEALQKQMDS 714


RESULT 4
ABM83671
ID   ABM83671 standard; protein; 1199 AA.
XX
AC   ABM83671;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:3920.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS   Homo sapiens.
XX
PN   WO2004023973-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Schmidt JP,  Wright RJ,  Bruns CM,  Marjanovic MM,  Shen F;
PI   Harthshorne TA,  Suchorolski MT,  Altus CM,  Pitts SJ,  Elder LV;
PI   Mooney EM,  Delegeane AM,  Panesar IS,  Banville SC,  Reddy TP;
PI   Stevens KA,  Blanchard JL,  Panzer SR,  Wang X,  Au AP,  Gerstin EH;
PI   Peralta CH,  Anderson SB,  Rioux P,  Shen EJ,  Wu MC,  Stuve LL;
PI   Lagace RE,  Spiro PA,  Stewart EA,  Wingrove J,  Vitt UA,  Kirton ES;
PI   Xu Y,  Kwong M,  Policky JL,  Hurwitz BL,  Ma Y,  Jackson JL,  Gietzen D;
PI   Patury S,  Shi X,  Suarez CJ;
XX
DR   WPI; 2004-329368/30.
DR   N-PSDB; ACN42323.
XX
PT   New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT   in gene mapping.
XX
PS   Claim 27; Page; 190pp; English.
XX
CC   The invention relates to novel diagnostic and therapeutic polynucleotides
CC   selected from one of the 2722 sequences defined in the specification. A
CC   polynucleotide of the invention may have a use in gene therapy. The human
CC   diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC   used to diagnose a particular condition, disease or disorder associated
CC   with human molecules, e.g. cell proliferative disorders,
CC   autoimmune/inflammatory disorder, developmental disorder, endocrine
CC   disorder, neurological disorders, gastrointestinal disorders, or
CC   infections caused by virus, bacteria, fungi or parasite. The dithp
CC   molecules may also be used in genetic mapping, in identifying individuals
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp protein of the
CC   invention. Note: The sequence data for this patent is not represented in
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX

SQ   Sequence 1199 AA;

  Query Match             41.7%;  Score 1679;  DB 8;  Length 1199;
  Best Local Similarity   41.8%;  Pred. No. 9.8e-119;
  Matches  385;  Conservative  139;  Mismatches  232;  Indels  164;  Gaps   21;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63

Db          3 GASVKVAVRVRPFNSRETSKESKCIIQMQGNSTSIINPKNPKE----------APKSFS 51

Qy         64 FDRSYWSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122

Db         52 FDYSYWSHTSPEDPCFASQNRVYNDIGKEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGKQ 111

Qy        123 KEH--GVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180

Db        112 EESQAGIIPQLCEELFEKIND-NCNEEMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE 170

Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240

Db        171 HPLLGPYVEDLSKLAVTSYTDIADLMDAGNKARTVAATNMNETSSRSHAVFTIVFTQKKH 230

Qy        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM-- 298

Db        231 DNETNLSTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEVDN 290

Qy        299 ---SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADS 355

Db        291 CTSKSKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADR 350

Qy        356 AKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGG-----------GGAG----- 399

Db        351 AKQIKCNAVINEDPNAKLVRELKEEVTRLKDLLRAQGLGDIIDIDPLIDDYSGSGSKYLK 410

Qy        400 ----------------------GSGGPVEESYPPDTPLEKQ-----IVSIQQPDATVKK 431

Db        411 DFQNNKHRYLLASENQRPGHFSTASMGSLTSS-PSSCSLSSQVGLTSVTSIQ--ERIMST 467

Qy        432 MSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISIEK--GFVGPYH 489

Db        468 PGGEEAIERLKESEKIIAELNETWEEKLRKTEAIRMEREALLAEMGVAIREDGGTLGVFS 527

Qy        490 SKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKILKEHCTFENV- 548

Db        528 PKKTPHLVNLNEDPLMSECLLYYIKDGITRVGQADAERRQDIVLSGAHIKEEHCIFRSER 587

Qy        549 ----DNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHPEEARAER--- 601

Db        588 SNSGEVIVTLEPCERSETYVNGKRVSQPVQLRSGNRIIMGKNHVFRFNHPEQARAEREKT 647

Qy        602 ---------------QEQSLLRHSVTNSQ-----------LGSPAPGRHDRTLSKAGSDA 635

Db        648 PSAETPSEPVDWTFAQRELLEKQGIDMKQEMEKRLQEMEILYKKEKEEADLLLEQQRLDA 707

Qy        636 DGDSRSDS-------------------------------------------------PLPHFR 649

Db        708 DSDSGDDSDKRSCEESWKLITSLREKLPPSKLQTIVKKCGLPSSGKKREPIKMYQIPQRR 767

Qy        650 --GKDSDWFYARREAASAILGLDQKISHLTD-----DELDALFDDVQKARAVRRGLVEDN 702

Db        768 RLSKDSKWVTISDLKIQAVKEICYEVA-LNDFRHSRQEIEALAIVKMKELCAMYGKKDPN 826

Qy        703 EDSDSQSSFPVRDKYMSNGTIDNFSLDTAITMPGTPRSDD-----DGDALFFGDKKSKQD 757

Db        827 E-RDSWRAV-ARDVWDTVGVGDEKIEDVMATGKGSTDVDDLKVHIDKLEDILQEVKKQNN 884

Qy        758 ASNVDVEELRQQQAQMEEAL 777

Db        885 MKDEEIKVLRNKMLKMEKVL 904


RESULT 5
ABM83653
```

ID ABM83653 standard; protein; 1696 AA.
XX
AC ABM83653;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3902.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
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PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI; 2004-329368/30.
DR N-PSDB; ACN42305.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
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XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
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CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 1696 AA;

Query Match 41.6%; Score 1674.5; DB 8; Length 1696;
Best Local Similarity 46.4%; Pred. No. 3.7e-118;
Matches 356; Conservative 128; Mismatches 175; Indels 109; Gaps 16;

```
Qy          4 GGNIKVVVRVRPFNARE IDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||: | :|||::| |: | :   |   :|            ||:|:
Db          3 GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET----------PKSFS 51

Qy         64 FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
              || ||||    :|   ||| |: :::|:|  :| :||:||| ||||||||||:|||:|||
Db         52 FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG 109

Qy        121 YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
                :  : |:||::|:|:| |||:   | |:: :|||||:||| |||||||||  ||||:|
Db        110 KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV 168

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
              ||||  |||||||:|| | |: :|::||| |||||||||||||||||||||||| :  |||
Db        169 REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK 228

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
              || || : ||||:|||||||||||| |||| | |||||| ||:||:|||:||:|||:|
Db        229 RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM 288

Qy        299 ---SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADS 355
                  : |:||   :||||||||||:::||||| |||:||:|||||::|||||||||
Db        289 XPPQNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADR 348

Qy        356 AKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGG--------GGAG-------- 399
              ||:|: :||:|||| ::|||||:|: :||  | : | |         ||
Db        349 AKQIRCNAVINEDPNNKLIRELKDEVTRLRDLLYAQGLGDITDTNTVPGGPKYVSDLENN 408

Qy        400 --GSGGPVEESYPPDTPLEKQIVSIQQPDATVKKMS----------------KAEIVE 439
                || | |:  | : :   :| :  | ::: :|                  | :|
Db        409 NLNRGGTVNEAPDPLSTVTNALVGM-SPSSSLSALSSRAASVSSLHERILFAPGSEEAIE 467

Qy        440 QLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISIEK--GFVGPYHSKEMPHLV 497
              :| ::||:  :||:|||||| :|| |  |||| | |:|::: :  | :| :  |: ||||
Db        468 RLKETEKIIAELNETWEEKLRRTEAIRMEREALLAEMGVAMREDGGTLGVFSPKKTPHLV 527

Qy        498 NLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKILKEHCTFEN-----VDNVV 552
              ||::|||::|||:| || | |||| : : : :| |:|  | :||| | :    : ||
Db        528 NLNEDPLMSECLLYYIKDGITRVGREDGERRQDIVLSGHFIKEEHCVFRSDSRGGSEAVV 587

Qy        553 TIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHPEEARAERQEQSLLRHSVT 612
              |: | | |   ||| :: :|: |||| |||:|  |:|||||||:|| ||:
Db        588 TLEPCEGADTYVNGKKVTEPSILRSGNRIIMGKSHVFRFNHPEQARQERER--------- 638

Qy        613 NSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHFRGKDSDWFYARREAASAILGLDQK 672
                                                :|      :  || :|:||      |:| |
Db        639 ------------------------------TPCAETPAEPVDWAFAQRELLEK-QGIDMK 667

Qy        673 ISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDSQSSFPVRDKYMSN 720
                  :  | | |  :: |     |:|  :  | :|     | | :
Db        668 --QEMEQRLQELEDQYRRERREEATYLLE-QQRLDYESKLEALQKQMDS 712
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RESULT 6
ABM83649
ID ABM83649 standard; protein; 1709 AA.
XX
AC ABM83649;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3898.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI; 2004-329368/30.
DR N-PSDB; ACN42301.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 1709 AA;

Query Match 41.6%; Score 1674.5; DB 8; Length 1709;
Best Local Similarity 46.4%; Pred. No. 3.7e-118;
Matches 356; Conservative 128; Mismatches 175; Indels 109; Gaps 16;

```
Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||: | :|||::| |: | :   |    :|            ||:|:
Db          3 GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET----------PKSFS 51

Qy         64 FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
              || ||||    :|   ||| |: :::|:|  :| :||:||| ||||||||:||||:|||
Db         52 FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG 109

Qy        121 YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
               :  : |:||::|:|:| |||:   | |:: :|||||:||| |||||||||  ||||:|
Db        110 KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV 168

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
              ||||  |||||||:|| | |: :|::||| ||||||||||||||||||||| :  |||
Db        169 REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK 228

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
               || || : ||||:|||||||||||||| |||| | |||||| ||:||:|||:||:|||:|
Db        229 RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM 288

Qy        299 ---SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADS 355
                 : |:||   :|||||||||||:::||||| |||:||:||||||::||||||||||
Db        289 XPPQNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADR 348

Qy        356 AKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGG--------GGAG-------- 399
              ||:|: :||:|||| ::|||||:|: :||   | : | |          ||
Db        349 AKQIRCNAVINEDPNNKLIRELKDEVTRLRDLLYAQGLGDITDTNTVPGGPKYVSDLENN 408

Qy        400 --GSGGPVEESYPPDTPLEKQIVSIQQPDATVKKMS----------------KAEIVE 439
                || | |:  | : :   :| :  | ::: :|                    | :|
Db        409 NLNRGGTVNEAPDPLSTVTNALVGM-SPSSSLSALSSRAASVSSLHERILFAPGSEEAIE 467

Qy        440 QLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISIEK--GFVGPYHSKEMPHLV 497
              :| ::||:  :||:|||||| :|| |  |||| | |:|::: :  | :| :  |: ||||
```

Db 468 RLKETEKIIAELNETWEEKLRRTEAIRMEREALLAEMGVAMREDGGTLGVFSPKKTPHLV 527

Qy 498 NLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKILKEHCTFEN-----VDNVV 552
||::|||::|||:| || | |||| : : : :| |:| | :||| | : : ||
Db 528 NLNEDPLMSECLLYYIKDGITRVGREDGERRQDIVLSGHFIKEEHCVFRSDSRGGSEAVV 587

Qy 553 TIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHPEEARAERQEQSLLRHSVT 612
|: | | | ||| :: :|: |||| |||:| |:|||||||:|| ||:
Db 588 TLEPCEGADTYVNGKKVTEPSILRSGNRIIMGKSHVFRFNHPEQARQERER--------- 638

Qy 613 NSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHFRGKDSDWFYARREAASAILGLDQK 672
:| : || :|:|| |:| |
Db 639 ----------TPCAETPAEPVDWAFAQRELLEK-QGIDMK 667

Qy 673 ISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDSQSSFPVRDKYMSN 720
: | | | :: | |:| : | :| | | :
Db 668 --QEMEQRLQELEDQYRREREEATYLLE-QQRLDYESKLEALQKQMDS 712

RESULT 7
ABM83646
ID ABM83646 standard; protein; 1722 AA.
XX
AC ABM83646;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3895.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI; 2004-329368/30.
DR N-PSDB; ACN42298.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals

```
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp protein of the
CC   invention. Note: The sequence data for this patent is not represented in
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 1722 AA;

  Query Match            41.6%;  Score 1674.5;  DB 8;  Length 1722;
  Best Local Similarity  46.4%;  Pred. No. 3.8e-118;
  Matches  356;  Conservative  128;  Mismatches  175;  Indels  109;  Gaps   16;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||: | :|||::| |: | :  |   :|            ||:|:
Db          3 GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET----------PKSFS 51

Qy         64 FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
              || ||||    :|   ||| |: :::|:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG 109

Qy        121 YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
               :  : |:||::|:|:| |||:   | |:: :|||||:||| |||||||| ||||:|
Db        110 KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV 168

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
              ||||  |||||||:|| | |: :|::||| |||||||||||||||||||||||| :  |||
Db        169 REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK 228

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
              || || : ||||:|||||||||||||| |||| | |||||| ||:||:|||:||:|||:|
Db        229 RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM 288

Qy        299 ---SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADS 355
                 : |:||   :|||||||||||:::|||||  |||:||:|||||::|||||||||
Db        289 XPPQNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADR 348

Qy        356 AKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGG--------GGAG-------- 399
              ||:|: :||:|||||  ::|||||:|: :||  | : | |          ||
Db        349 AKQIRCNAVINEDPNNKLIRELKDEVTRLRDLLYAQGLGDITDTNTVPGGPKYVSDLENN 408

Qy        400 --GSGGPVEESYPPDTPLEKQIVSIQQPDATVKKMS-----------------KAEIVE 439
                || | |:  | : :   :| :  | :::  :|                   | :|
Db        409 NLNRGGTVNEAPDPLSTVTNALVGM-SPSSSLSALSSRAASVSSLHERILFAPGSEEAIE 467

Qy        440 QLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISIEK--GFVGPYHSKEMPHLV 497
              :| ::||:  :||:|||||| :|| |  |||| | |:|::: :  | :| :  |: ||||
Db        468 RLKETEKIIAELNETWEEKLRRTEAIRMEREALLAEMGVAMREDGGTLGVFSPKKTPHLV 527

Qy        498 NLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKILKEHCTFEN-----VDNVV 552
              ||::|||::|||:| || | |||| : : : :| |:|  | :||| | :      : ||
Db        528 NLNEDPLMSECLLYYIKDGITRVGREDGERRQDIVLSGHFIKEEHCVFRSDSRGGSEAVV 587

Qy        553 TIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHPEEARAERQEQSLLRHSVT 612
              |: | | |   ||| :: :|: |||| |||:|  |:|||||:|| ||:
Db        588 TLEPCEGADTYVNGKKVTEPSILRSGNRIIMGKSHVFRFNHPEQARQERER--------- 638

Qy        613 NSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHFRGKDSDWFYARREAASAILGLDQK 672
                                      :|      :  || :|:||      |:| |
Db        639 ----------------------------TPCAETPAEPVDWAFAQRELLEK-QGIDMK 667

Qy        673 ISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDSQSSFPVRDKYMSN 720
                :  | | |  :: |     |:|  :  | :|       | | :
Db        668 --QEMEQRLQELEDQYRRREREEATYLLE-QQRLDYESKLEALQKQMDS 712


RESULT 8
ABM83650
ID   ABM83650 standard; protein; 1708 AA.
XX
AC   ABM83650;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:3899.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS   Homo sapiens.
XX
PN   WO2004023973-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Schmidt JP,  Wright RJ,  Bruns CM,  Marjanovic MM,  Shen F;
PI   Harthshorne TA,  Suchorolski MT,  Altus CM,  Pitts SJ,  Elder LV;
PI   Mooney EM,  Delegeane AM,  Panesar IS,  Banville SC,  Reddy TP;
PI   Stevens KA,  Blanchard JL,  Panzer SR,  Wang X,  Au AP,  Gerstin EH;
PI   Peralta CH,  Anderson SB,  Rioux P,  Shen EJ,  Wu MC,  Stuve LL;
PI   Lagace RE,  Spiro PA,  Stewart EA,  Wingrove J,  Vitt UA,  Kirton ES;
PI   Xu Y,  Kwong M,  Policky JL,  Hurwitz BL,  Ma Y,  Jackson JL,  Gietzen D;
PI   Patury S,  Shi X,  Suarez CJ;
XX
DR   WPI; 2004-329368/30.
DR   N-PSDB; ACN42302.
XX
PT   New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT   in gene mapping.
XX
PS   Claim 27; Page; 190pp; English.
XX
CC   The invention relates to novel diagnostic and therapeutic polynucleotides
CC   selected from one of the 2722 sequences defined in the specification. A
CC   polynucleotide of the invention may have a use in gene therapy. The human
CC   diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC   used to diagnose a particular condition, disease or disorder associated
CC   with human molecules, e.g. cell proliferative disorders,
CC   autoimmune/inflammatory disorder, developmental disorder, endocrine
CC   disorder, neurological disorders, gastrointestinal disorders, or
CC   infections caused by virus, bacteria, fungi or parasite. The dithp
CC   molecules may also be used in genetic mapping, in identifying individuals
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp protein of the
CC   invention. Note: The sequence data for this patent is not represented in
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 1708 AA;

  Query Match            41.5%;  Score 1673;  DB 8;  Length 1708;
  Best Local Similarity  46.9%;  Pred. No. 4.9e-118;
  Matches  353;  Conservative  124;  Mismatches  175;  Indels  100;  Gaps   14;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||: | :|||::| |: | :  |   :|            ||:|:
Db          3 GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET----------PKSFS 51

Qy         64 FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
              || ||||    :|   ||| |: :::|:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG 109

Qy        121 YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
               :  : |:||::|:|:| |||:   | |:: :|||||:||| |||||||| ||||:|
Db        110 KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV 168

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
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Db        169 REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK 228

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298

Db        229 RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM 288

Qy        299 SSG-----KQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYA 353

Db        289 DSGPNKNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYA 348

Qy        354 DSAKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGAGGSGGPVEESYPPDT 413

Db        349 DRAKQIRCNAVINEDPNNKLIRELKDEVTRLRDLLY--------AQGLGDITDTNTVPGG 400

Qy        414 PLEKQIVSIQQPDATVKKMS-----------------KAEIVEQLNQSEKLYRDLNQTW 455

Db        401 PKLTNALVGMSPSSSLSALSSRAASVSSLHERILFAPGSEEAIERLKETEKIIAELNETW 460

Qy        456 EEKLAKTEEIHKEREAALEELGISIEK--GFVGPYHSKEMPHLVNLSDDPLLAECLVYNI 513

Db        461 EEKLRRTEAIRMEREALLAEMGVAMREDGGTLGVFSPKKTPHLVNLNEDPLMSECLLYYI 520

Qy        514 KPGQTRVGNVNQDTQAEIRLNGSKILKEHCTFEN-----VDNVVTIVPNEKAAVMVNGVR 568

Db        521 KDGITRVGREDGERRQDIVLSGHFIKEEHCVFRSDSRGGSEAVVTLEPCEGADTYVNGKK 580

Qy        569 IDKPTRLRSGYRIILGDFHIFRFNHPEEARAERQEQSLLRHSVTNSQLGSPAPGRHDRTL 628

Db        581 VTEPSILRSGNRIIMGKSHVFRFNHPEQARQERER------------------------ 615

Qy        629 SKAGSDADGDSRSDSPLPHFRGKDSDWFYARREAASAILGLDQKISHLTDDELDALFDDV 688

Db        616 --------------TPCAETPAEPVDWAFAQRELLEK-QGIDMK--QEMEQRLQELEDQY 658

Qy        689 QKARAVRRGLVEDNEDSDSQSSFPVRDKYMSN 720

Db        659 RREREEATYLLE-QQRLDYESKLEALQKQMDS 689


RESULT 9
ABM83651
ID   ABM83651 standard; protein; 1699 AA.
XX
AC   ABM83651;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:3900.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS   Homo sapiens.
XX
PN   WO2004023973-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Schmidt JP,  Wright RJ,  Bruns CM,  Marjanovic MM,  Shen F;
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PI   Stevens KA,  Blanchard JL,  Panzer SR,  Wang X,  Au AP,  Gerstin EH;
PI   Peralta CH,  Anderson SB,  Rioux P,  Shen EJ,  Wu MC,  Stuve LL;
PI   Lagace RE,  Spiro PA,  Stewart EA,  Wingrove J,  Vitt UA,  Kirton ES;
PI   Xu Y,  Kwong M,  Policky JL,  Hurwitz BL,  Ma Y,  Jackson JL,  Gietzen D;
PI   Patury S,  Shi X,  Suarez CJ;
XX
DR   WPI; 2004-329368/30.
DR   N-PSDB; ACN42303.
XX
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PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
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CC   with human molecules, e.g. cell proliferative disorders,
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CC   disorder, neurological disorders, gastrointestinal disorders, or
CC   infections caused by virus, bacteria, fungi or parasite. The dithp
CC   molecules may also be used in genetic mapping, in identifying individuals
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp protein of the
CC   invention. Note: The sequence data for this patent is not represented in
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 1699 AA;

  Query Match             41.4%;  Score 1669.5;  DB 8;  Length 1699;
  Best Local Similarity   46.8%;  Pred. No. 8.9e-118;
  Matches  352;  Conservative  125;  Mismatches  166;  Indels  109;  Gaps   15;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63

Db          3 GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET-----------PKSFS 51

Qy         64 FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120

Db         52 FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG 109

Qy        121 YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178

Db        110 KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV 168

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238

Db        169 REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK 228

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298

Db        229 RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM 288

Qy        299 SSG-----KQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYA 353

Db        289 DSGPNKNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYA 348

Qy        354 DSAKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGAGGSGGPVEESYPPDT 413

Db        349 DRAKQIRCNAVINEDPNNKLIRELKDEVTRLRDLLYAQGLG---------------DIT 392

Qy        414 PLEKQIVSIQQPDATVKKMS-----------------KAEIVEQLNQSEKLYRDLNQTW 455

Db        393 DMTNALVGM-SPSSSLSALSSRAASVSSLHERILFAPGSEEAIERLKETEKIIAELNETW 451

Qy        456 EEKLAKTEEIHKEREAALEELGISIEK--GFVGPYHSKEMPHLVNLSDDPLLAECLVYNI 513

Db        452 EEKLRRTEAIRMEREALLAEMGVAMREDGGTLGVFSPKKTPHLVNLNEDPLMSECLLYYI 511

Qy        514 KPGQTRVGNVNQDTQAEIRLNGSKILKEHCTFEN-----VDNVVTIVPNEKAAVMVNGVR 568

Db        512 KDGITRVGREDGERRQDIVLSGHFIKEEHCVFRSDSRGGSEAVVTLEPCEGADTYVNGKK 571
```

```
Qy        569 IDKPTRLRSGYRIILGDFHIFRFNHPEEARAERQEQSLLRHSVTNSQLGSPAPGRHDRTL 628
Db        572 VTEPSILRSGNRIIMGKSHVFRFNHPEQARQERER------------------------ 606

Qy        629 SKAGSDADGDSRSDSPLPHFRGKDSDWFYARREAASAILGLDQKISHLTDDELDALFDDV 688
Db        607 -------------TPCAETPAEPVDWAFAQRELLEK-QGIDMK--QEMEQRLQELEDQY 649

Qy        689 QKARAVRRGLVEDNEDSDSQSSFPVRDKYMSN 720
Db        650 RREREEATYLLE-QQRLDYESKLEALQKQMDS 680


RESULT 10
AAB36227
ID   AAB36227 standard; protein; 1816 AA.
XX
AC   AAB36227;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Human kinesin-like protein HKLP SEQ ID NO: 4.
XX
KW   Human; kinesin-like protein; HKLP; KIF1; cell division; cancer;
KW   intracellular transport; neurological disorder; infertility;
KW   biallelic marker; spontaneous abortion; neonatal chromosome disorder;
KW   aneuploidy.
XX
OS   Homo sapiens.
XX
PN   WO200063375-A1.
XX
PD   26-OCT-2000.
XX
PF   20-APR-2000; 2000WO-IB000562.
XX
PR   20-APR-1999;   99US-0130217P.
XX
PA   (GEST ) GENSET.
XX
PI   Bougueleret L,  Dufaure-Gare I,  Grel P;
XX
DR   WPI; 2000-665242/64.
DR   N-PSDB; AAC66550.
XX
PT   An isolated or purified human kinesin-like protein (HKLP) encoding
PT   polynucleotide used to detect HKLP polynucleotides in a sample comprises
PT   a contiguous span of at least 12 nucleotides.
XX
PS   Claim 46; Page 189-192; 199pp; English.
XX
CC   The present invention describes the coding and protein sequences of the
CC   human kinesin-like protein HKLP. It is thought that the protein could be
CC   involved in neurological disorders, infertility, spontaneous abortion,
CC   neonatal chromosome disorders, aneuploidy and cancers. This is due to its
CC   function in the movement of microtubules. The protein shows homology to
CC   the murine KIF1A and KIF1B proteins. The sequences disclosed in the
CC   invention can be used in the isolation of similar human proteins and in
CC   vector production. In addition, the biallelic markers shown can be used
CC   in disease diagnosis and population studies
XX
SQ   Sequence 1816 AA;

  Query Match             41.4%;  Score 1668.5;  DB 3;  Length 1816;
  Best Local Similarity   45.0%;  Pred. No. 1.2e-117;
  Matches  356;  Conservative  126;  Mismatches  172;  Indels  137;  Gaps   16;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
Db          3 GASVKVAVRVRPFNSRETSKESKCIIQMQGNSTSIINPKNPKE----------APKSFS 51

Qy         64 FDRSYWSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122
Db         52 FDYSYWSHTSPEDPCFASQNRVYNDIGKEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGKQ 111

Qy        123 KEH--GVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
Db        112 EESQAGIIPQLCEELFEKIND-NCNEEMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE 170

Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240
Db        171 HPLLGPYVEDLSKLAVTSYTDIADLMDAGNKARTVAATNMNETSSRSHAVFTIVFTQKKH 230

Qy        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM-- 298
Db        231 DNETNLSTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEVDN 290

Qy        299 ---SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADS 355
Db        291 CTSKSKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADR 350

Qy        356 AKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGG-----------GGAG----- 399
Db        351 AKQIKCNAVINEDPNAKLVRELKEEVTRLKDLLRAQGLGDIIDIDPLIDDYSGSGSKYLK 410

Qy        400 ----------------------GSGGPVEESYPPDTPLEKQ-----IVSIQQPDATVKK 431
Db        411 DFQNNKHRYLLASENQRPGHFSTASMGSLTSS-PSSCSLSSQVGLTSVTSIQ--ERIMST 467

Qy        432 MSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISIEK--GFVGPYH 489
Db        468 PGGEEAIERLKESEKIIAELNETWEEKLRKTEAIRMEREALLAEMGVAIREDGGTLGVFS 527

Qy        490 SKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKILKEHCTFENV- 548
Db        528 PKKTPHLVNLNEDPLMSECLLYYIKDGITRVGQADAERRQDIVLSGAHIKEEHCIFRSER 587

Qy        549 ----DNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHPEEARAERQEQ 604
Db        588 SNSGEVIVTLEPCERSETYVNGKRVSQPVQLRSGNRIIMGKNHVFRFNHPEQARAEREK- 646

Qy        605 SLLRHSVTNSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHFRGKDSDWFYARREAAS 664
Db        647 ------------------------------------TPSAETPSEPVDWTFAQRELLE 668

Qy        665 AILGLDQK------------ISHLTDDELDALFDD-----------VQKARAVRRGLVED 701
Db        669 K-QGIDMKQEMEKRLQEMEILYKKEKEEADLLLEQQRLDYESKLQALQKQVETRSLAAET 727

Qy        702 NEDSDSQSSFP 712
Db        728 TEEEEEEEEVP 738


RESULT 11
ADJ95088
ID   ADJ95088 standard; protein; 1805 AA.
XX
AC   ADJ95088;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Novel NOVX protein sequence #158.
XX
KW   antidiabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic;
KW   anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic;
KW   neuroprotective; antiparkinsonian; anticonvulsant; osteopathic;
KW   antiarthritic; antiinflammatory; dermatological; antiasthmatica;
KW   antilipemic; gene therapy; metabolic disorder; diabetes; obesity;
KW   infectious disease; anorexia; cancer; cardiovascular disease;
KW   hypertension; atherosclerosis; neurodegenerative disorder;
KW   Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;
KW   osteoarthritis; hematopoietic disorder; inflammatory skin disorder;
KW   asthma; dyslipidemia; neurogenesis; cell differentiation;
KW   cell proliferation; hematopoiesis; wound healing; angiogenesis;
```

KW chromosome mapping; tissue typing; pharmacogenomic.
XX
OS Homo sapiens.
XX
PN WO2003040325-A2.
XX
PD 15-MAY-2003.
XX
PF 05-NOV-2002; 2002WO-US035464.
XX
PR 05-NOV-2001; 2001US-0338626P.
PR 06-NOV-2001; 2001US-0333072P.
PR 09-NOV-2001; 2001US-0348283P.
PR 15-NOV-2001; 2001US-0335610P.
PR 16-NOV-2001; 2001US-0338543P.
PR 20-NOV-2001; 2001US-0331630P.
PR 20-NOV-2001; 2001US-0331641P.
PR 21-NOV-2001; 2001US-0332152P.
PR 27-NOV-2001; 2001US-0333461P.
PR 28-NOV-2001; 2001US-0333912P.
PR 28-NOV-2001; 2001US-0334027P.
PR 29-NOV-2001; 2001US-0334300P.
PR 30-NOV-2001; 2001US-0334421P.
PR 30-NOV-2001; 2001US-0334526P.
PR 04-DEC-2001; 2001US-0336576P.
PR 04-DEC-2001; 2001US-0336664P.
PR 07-DEC-2001; 2001US-0338314P.
PR 07-DEC-2001; 2001US-0338390P.
PR 10-DEC-2001; 2001US-0339006P.
PR 10-DEC-2001; 2001US-0339008P.
PR 11-DEC-2001; 2001US-0339286P.
PR 01-FEB-2002; 2002US-0353280P.
PR 01-FEB-2002; 2002US-0353288P.
PR 04-FEB-2002; 2002US-0354392P.
PR 04-FEB-2002; 2002US-0354393P.
PR 04-FEB-2002; 2002US-0354409P.
PR 27-FEB-2002; 2002US-0359944P.
PR 27-FEB-2002; 2002US-0360148P.
PR 05-MAR-2002; 2002US-0361790P.
PR 05-MAR-2002; 2002US-0361833P.
PR 05-MAR-2002; 2002US-0361925P.
PR 05-MAR-2002; 2002US-0362230P.
PR 05-MAR-2002; 2002US-0362625P.
PR 13-MAR-2002; 2002US-0364000P.
PR 13-MAR-2002; 2002US-0364181P.
PR 13-MAR-2002; 2002US-0364182P.
PR 13-MAR-2002; 2002US-0364197P.
PR 13-MAR-2002; 2002US-0364227P.
PR 17-MAY-2002; 2002US-0381621P.
PR 28-MAY-2002; 2002US-0383675P.
PR 17-JUL-2002; 2002US-0396703P.
PR 06-AUG-2002; 2002US-0401552P.
PR 07-AUG-2002; 2002US-0401594P.
PR 07-AUG-2002; 2002US-0401787P.
PR 15-AUG-2002; 2002US-0403619P.
PR 20-AUG-2002; 2002US-0404821P.
PR 23-AUG-2002; 2002US-0405368P.
PR 23-AUG-2002; 2002US-0405402P.
PR 23-AUG-2002; 2002US-0405496P.
PR 23-AUG-2002; 2002US-0405631P.
PR 26-AUG-2002; 2002US-0406125P.
PR 04-NOV-2002; 2002US-00287226.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Agee ML, Alsobrook JP, Berghs C, Boldog FL, Burgess CE, Chant JS;
PI Chaudhuri A, Dipippo VA, Edinger SR, Eisen A, Ellerman K;
PI Gangolli EA, Gorman L, Gerlach VL, Ji W, Kekuda R, Khramtsov NV;
PI Li L, Malyankar UM, Macdougall JR, Mezes PS, Miller CE, Millet I;
PI Ooi CE, Ort T, Padigaru M, Patturajan M, Rastelli L, Rieger DK;
PI Rothenberg ME, Shenoy SG, Spaderna SK, Spytek KA, Taupier RJ;
PI Vernet CAM, Zerhusen BD, Zhong M;
XX

DR WPI; 2003-441551/41.
DR N-PSDB; ADJ95087.
XX
PT New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX
PS Claim 1; SEQ ID NO 316; 800pp; English.
XX
CC The invention relates to novel isolated polypeptides, mature forms of
CC these, or a sequence that is at least 95 % identical to, or having one or
CC more conservative amino acid substitutions in the polypeptides. The
CC polypeptides, nucleic acid molecules and antibodies are useful in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease, preferably a NOVX-associated disorder. The nucleic acid
CC molecules, polypeptides and antibodies are useful for treating,
CC preventing or diagnosing diseases such metabolic disorders, diabetes,
CC obesity, infectious diseases (viral, bacterial, fungal, helminthic, and
CC protozoal), anorexia, cancer, cardiovascular diseases (hypertension,
CC atherosclerosis), neurodegenerative disorders, Alzheimer's disease,
CC Parkinson's disease, epilepsy, immune disorders (osteoarthritis),
CC hematopoietic disorders, inflammatory skin disorders, asthma, and various
CC dyslipidemias. The nucleic acids and polypeptides may also be used as
CC targets for the identification of small molecules that modulate or
CC inhibit e.g. neurogenesis, cell differentiation, cell proliferation,
CC hematopoiesis, wound healing and angiogenesis, in gene therapy, in
CC generation of antibodies that bind immunospecifically to NOVX substances
CC for use in therapeutic or diagnostic methods. The nucleic acids are
CC further used as hybridization probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. This sequence
CC corresponds to one of the NOVX polypeptides of the invention.
XX
SQ Sequence 1805 AA;

Query Match 41.4%; Score 1667.5; DB 7; Length 1805;
Best Local Similarity 45.2%; Pred. No. 1.4e-117;
Matches 355; Conservative 127; Mismatches 172; Indels 131; Gaps 16;

```
Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||  : :|||::|:|| | :  |   :|           ||:|:
Db          3 GASVKVAVRVRPFNSRETSKESKCIIQMQGNSTSIINPKNPKE----------APKSFS 51

Qy         64 FDRSYWSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122
              || ||||      | :| |  :: |:|  :| :||:||| ||||||||||:||||:|||
Db         52 FDYSYWSHTSPEDPCFASQNRVYNDIGKEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGKQ 111

Qy        123 KEH--GVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
              :|   |:||::|:::| :||:   :: :: :|||||:||| |||||||||  ||||:|||
Db        112 EESQAGIIPQLCEELFEKIND-NCNEEMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE 170

Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240
              ||  |||||||:|| | |: :| :||| ||||||||||||||||||||||:  ||| |
Db        171 HPLLGPYVEDLSKLAVTSYTDIADLMDAGNKARTVAATNMNETSSRSHAVFTIVFTQKKH 230

Qy        241 DEETKMDTEK-VAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMS 299
              | || : ||| |:|||||||||||||| |||| | |||||| ||:||:|||:||:|||::|
Db        231 DNETNLSTEKVVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEVS 290

Qy        300 SGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKRI 359
              |:||   :|||||||||||:::||||| |||:||:||||||::|||||||||| ||:|
Db        291 K-KKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADRAKQI 349

Qy        360 KNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGG--------GGAGGSGGPVEE---- 407
              | :||:||||||:::|||||: :|:  |:: | |             |||  :::
Db        350 KCNAVINEDPNAKLVRELKEEVTRLKDLLRAQGLGDIIDVDPLIDDYSGSGSKLKDFQNN 409

Qy        408 ------------------------SYPPDTPLEKQ-----IVSIQQPDATVKKMSKAEI 437
                                       | |    | |     : |||  :  :      |
Db        410 KHRYLLASENQRPGHFSTASMGSLTSSPSSCSLSSQVGLTSVTSIQ--ERIMSTPGGEEA 467

Qy        438 VEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISIEK--GFVGPYHSKEMPH 495
              :|:| :|||:  :||:|||||| ||| |  |||| | |:|::| :  | :| :  |: ||
```

```
Db        468 IERLKESEKIIAELNETWEEKLRKTEAIRMEREALLAEMGVAIREDGGTLGVFSPKKTPH 527

Qy        496 LVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKILKEHCTFENV-----DN 550
              ||||::|||::|||:| || | ||||  : : : :| |:|: | :||| | :      :
Db        528 LVNLNEDPLMSECLLYYIKDGITRVGQADAERRQDIVLSGAHIKEEHCIFRSERSNSGEV 587

Qy        551 VVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHPEEARAERQEQSLLRHS 610
              :||: | |::   ||| |: :| :|||| |||:|  |:|||||||:|||||::
Db        588 IVTLEPCERSETYVNGKRVSQPVQLRSGNRIIMGKNHVFRFNHPEQARAEREK------- 640

Qy        611 VTNSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHFRGKDSDWFYARREAASAILGLD 670
                                                :|      :  || :|:||     |:|
Db        641 -------------------------------TPSAETPSEPVDWTFAQRELLEK-QGID 667

Qy        671 QK------------ISHLTDDELDALFDD-----------VQKARAVRRGLVEDNEDSDS 707
              |             :    :| | | :           :||    |    |  |: :
Db        668 MKQEMEKRLQEMEILYKKEKEEADLLLEQQRLDYESKLQALQKQVETRSLAAETTEEEEE 727

Qy        708 QSSFP 712
              :   |
Db        728 EEEVP 732
```

RESULT 12
AAE35317
ID AAE35317 standard; protein; 1770 AA.
XX
AC AAE35317;
XX
DT 17-JUN-2003 (first entry)
XX
DE Mouse KIF1Bbeta protein.
XX
KW KIF1Bb protein; gene therapy; molecular motor protein; kinesin; mouse;
KW kifB1beta gene-associated disease; Charcot-Marie-Tooth disease type 2A;
KW muscular; transgenic.
XX
OS Mus musculus.
XX
PN WO200297079-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-JP005226.
XX
PR 29-MAY-2001; 2001US-0293513P.
XX
PA (UYTY) UNIV TOKYO.
XX
PI Hirokawa N, Hayashi Y;
XX
DR WPI; 2003-167270/16.
DR N-PSDB; AAD53964.
XX
PT New KIF1Bb polypeptide having motor activity that transports synaptic
PT vesicle precursor, is useful for developing therapeutic or preventive
PT agent for kif1Bb gene-associated diseases e.g. Charcot-Marie-Tooth
PT disease type 2A.
XX
PS Claim 1; Page 72-78; 44pp; English.
XX
CC The invention relates to KIF1Bb protein which belongs to kinesin
CC superfamily of molecular motor proteins (KIFs). KIF1Bb is useful for
CC screening for a compound binding to it. Composition comprising the
CC selected compound is useful for treating, alleviating, or preventing a
CC kifB1beta gene-associated disease, in particular Charcot-Marie-Tooth
CC disease type 2A. Transgenic non-human vertebrate, are useful for
CC screening for a candidate compound for treating, alleviating, or
CC preventing a kif1Bbeta gene-associated disease. KIF1Bb DNA is useful for
CC gene therapy and for recombinant production of polypeptides. KIF1Bb
CC antibody is useful for affinity purification of KIF1Bb and for detecting
CC expression of kif1Bbeta gene at the protein level. The present sequence
CC is mouse KIF1Bbeta protein
XX
SQ Sequence 1770 AA;

Query Match 41.4%; Score 1666.5; DB 6; Length 1770;
Best Local Similarity 47.3%; Pred. No. 1.6e-117;
Matches 353; Conservative 125; Mismatches 174; Indels 95; Gaps 15;

```
Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:|| : :|||::|:|| | :  |   :|           ||:|:
Db          3 GASVKVAVRVRPFNSRETSKESKCIIQMQGNSTSIINPKNPKE----------APKSFS 51

Qy         64 FDRSYWSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122
              || ||||      | :| |  :: |:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWSHTSPEDPCFASQNRVYNDIGKEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGKQ 111

Qy        123 KEH--GVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
              :|   |:||::|:::| :||:   :: :: :|||||:||| |||||||||  ||||:|||
Db        112 EESQAGIIPQLCEELFEKIND-NCNEEMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE 170

Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240
              ||  |||||||:|| | |: :| :||| ||||||||||||||||||||||:  |||
Db        171 HPLLGPYVEDLSKLAVTSYTDIADLMDAGNKARTVAATNMNETSSRSHAVFTIVFTQKKQ 230

Qy        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS 300
              | || : ||||:|||||||||||||| |||| | |||||| ||:||:|||:||:|||::|
Db        231 DPETNLSTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEVSK 290

Qy        301 GKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKRIK 360
              |:||   :|||||||||||:::||||| |||:||:|||||||::||||||||| ||:||
Db        291 -KKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADRAKQIK 349

Qy        361 NHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGAGGSGGPVEESYPPDTPLEKQ-- 418
              :||:||||||:::|||||: :|:  |:: | |       |    | |    | |
Db        350 CNAVINEDPNAKLVRELKEEVTRLKDLLRAQGLGDIIDTSMGSLT--SSPSSCSLNSQVG 407

Qy        419 ---IVSIQQPDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEE 475
                : |||  :  :       | :|:| :|||:  :||:|||||| ||| |  |||| | |
Db        408 LTSVTSIQ--ERIMSTPGGEEAIERLKESEKIIAELNETWEEKLRKTEAIRMEREALLAE 465

Qy        476 LGISIEK--GFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRL 533
              :|::| :  | :| :  |:~||||||::|||::|||:| || | ||||  : : : :| |
Db        466 MGVAIREDGGTLGVFSPKKTPHLVNLNEDPLMSECLLYYIKDGITRVGQADAERRQDIVL 525

Qy        534 NGSKILKEHCTFENV-----DNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHI 588
              :|: | :||| | :      : :||: | |::   ||| |:  | :|||| |||:|  |:
Db        526 SGAHIKEEHCLFRSERSNTGEVIVTLEPCERSETYVNGKRVAHPVQLRSGNRIIMGKNHV 585

Qy        589 FRFNHPEEARAERQEQSLLRHSVTNSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHF 648
              |||||||:|||||::                                        :|
Db        586 FRFNHPEQARAEREK----------------------------------------TPSAET 606

Qy        649 RGKDSDWFYARREAASAILGLDQK------------ISHLTDDELDAL-----FDDVQKA 691
              :  || :|:||       |:| |             :  :| | |      |   |
Db        607 PSEPVDWTFAQRELLEK-QGIDMKQEMEKRLQEMEILYKKEKEEADLLLEQQRLDYESKL 665

Qy        692 RAVRRGL------VEDNEDSDSQSSFP 712
              :|::| :       |  |: : :   |
Db        666 QALQRQVETRSLAAETTEEEEEEEEVP 692
```

RESULT 13
ABB07867
ID ABB07867 standard; protein; 1823 AA.
XX
AC ABB07867;
XX
DT 03-JUL-2002 (first entry)
XX
DE Human kinesin-associated protein having motor domain.
XX
KW Human; kinesin-associated protein; motor domain; cytostatic; KIF1B-beta;
KW neuroblastoma.
XX

OS Homo sapiens.
XX
PN WO200226965-A1.
XX
PD 04-APR-2002.
XX
PF 01-OCT-2001; 2001WO-JP008635.
XX
PR 29-SEP-2000; 2000JP-00300247.
XX
PA (HISM) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
XX
PI Nakagawara A;
XX
DR WPI; 2002-340013/37.
DR N-PSDB; ABL40908.
XX
PT Gene encoding human kinesin-associated protein with motor domain, useful
PT for diagnosis and treatment of neuroblastoma.
XX
PS Claim 2; Page 40-48; 57pp; Japanese.
XX
CC The invention provides a human kinesin-associated gene encoding a protein
CC having a motor domain and another protein encoded by the human kinesin-
CC associated gene having no motor domain. The genes are useful for the
CC diagnosis and treatment of human neuroblastoma, and judgement of
CC prognosis of this disease. Also provided are probes and primers
CC hybridising to part of the KIF1B-beta gene, useful for diagnosing
CC neuroblastoma in which the gene sequence is detected in tissue samples.
CC The present sequence represents a human kinesin-associated protein having
CC the motor domain
XX
SQ Sequence 1823 AA;

Query Match 41.2%; Score 1661.5; DB 5; Length 1823;
Best Local Similarity 44.9%; Pred. No. 4.1e-117;
Matches 355; Conservative 126; Mismatches 173; Indels 137; Gaps 16;

```
Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||  : :|||::|:|| | :  |   :|           ||:|:
Db          3 GASVKVAVRVRPFNSRETSKESKCIIQMQGNSTSIINPKNPKE----------APKSFS 51

Qy         64 FDRSYWSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122
              || ||||      | :| |  :: |:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWSHTSPEDPCFASQNRVYNDIGKEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGKQ 111

Qy        123 KEH--GVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
              :|   |:||::|:::| :||:   :: :: :|||||:||| |||||||||  ||||:|||
Db        112 EESQAGIIPQLCEELFEKIND-NCNEEMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE 170

Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240
              ||  |||||||:|| | |: :| :||| ||||||||||||||||||||||:  ||| |
Db        171 HPLLGPYVEDLSKLAVTSYTDIADLMDAGNKARTVAATNMNETSSRSHAVFTIVFTQKKH 230

Qy        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM-- 298
              | || : ||||:|||||||||||||| |||| | |||||| ||:||:|||:||:|||::
Db        231 DNETNLSTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEVDN 290

Qy        299 ---SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADS 355
                | |:||   :|||||||||||:::|||||| |||:||:||||||::||||||||||
Db        291 CTSKSKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADR 350

Qy        356 AKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGG----------GGAG----- 399
              ||:|| :||:|| |||:::|||||| :|:  |:: | |            |:|
Db        351 AKQIKCNAVINEGPNAKLVRELKEEVTRLKDLLRAQGLGDIIDIDPLIDDYSGSGSKYLK 410

Qy        400 ----------------------GSGGPVEESYPPDTPLEKQ-----IVSIQQPDATVKK 431
                                   | | :  | |    | |     : |||  :  :
Db        411 DFQNNKHRYLLASENQRPGHFSTASMGSLTSS-PSSCSLSSQVGLTSVTSIQ--ERIMST 467

Qy        432 MSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISIEK--GFVGPYH 489
                  | :|:| :|||:  :||:|||||| ||| |  |||| | |:|::| :  | :| :
```

Db 468 PGGEEAIERLKESEKIIAELNETWEEKLRKTEAIRMEREALLAEMGVAIREDGGTLGVFS 527

Qy 490 SKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKILKEHCTFENV- 548
|: ||||||::|||::|||:| || | |||| : : : :| |:|: | :||| | :
Db 528 PKKTPHLVNLNEDPLMSECLLYYIKDGITRVGQADAERRQDIVLSGAHIKEEHCIFRSER 587

Qy 549 ----DNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHPEEARAERQEQ 604
: :||: | |:: ||| |: :| :|||| |||:| |:|||||||:|||||::
Db 588 SNSGEVIVTLEPCERSETYVNGKRVSQPVQLRSGNRIIMGKNHVFRFNHPEQARAEREK- 646

Qy 605 SLLRHSVTNSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHFRGKDSDWFYARREAAS 664
:| : || :|:||
Db 647 ----------TPSAETPSEPVDWTFAQRELLE 668

Qy 665 AILGLDQK-----------ISHLTDDELDALFDD----------VQKARAVRRGLVED 701
|:| | : :| | | : :|| | |
Db 669 K-QGIDMKQEMEKRLQEMEILYKKEKEEADLLLEQQRLDYESKLQALQKQVETRSLAAET 727

Qy 702 NEDSDSQSSFP 712
|: : : |
Db 728 TEEEEEEEEVP 738

RESULT 14
AAM40034
ID AAM40034 standard; protein; 893 AA.
XX
AC AAM40034;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 3179.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI59190.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Example 4; SEQ ID NO 3179; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the

CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 893 AA;

Query Match 41.2%; Score 1660.5; DB 4; Length 893;
Best Local Similarity 46.5%; Pred. No. 1.6e-117;
Matches 350; Conservative 126; Mismatches 167; Indels 109; Gaps 15;

```
Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||: | :|||::| |: | :  |   :|            ||:|:
Db          3 GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET----------PKSFS 51

Qy         64 FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
              || |||:   :|   ||| |: :::|:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWA--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG 109

Qy        121 YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
               :  : |:||::|:|:| |||:   | |:: :|||||:||| |||||||||  ||||:|
Db        110 KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV 168

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
              ||||  |||||||:|| | |: :|::||| ||||||||||||||||||||||| :  |||
Db        169 REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK 228

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
              || || : ||||:|||||||||||||| |||| | |||||| ||:||:|||:||:|||:|
Db        229 RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM 288

Qy        299 SSG-----KQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYA 353
              ||      |:||   :|||||||||||:::|||||  |||:||:||||||::|||||||||
Db        289 DSGPNKNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYA 348

Qy        354 DSAKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGAGGSGGPVEESYPPDT 413
              | ||:|: :||:||||| ::|||||:|: :||  | : | |                 |
Db        349 DRAKQIRCNAVINEDPNNKLIRELKDEVTRLRDLLYAQGLG---------------DIT 392

Qy        414 PLEKQIVSIQQPDATVKKMS-----------------KAEIVEQLNQSEKLYRDLNQTW 455
              :   :| :  | :::  :|                   | :|:| ::||:  :||:||
Db        393 DMTNALVGM-SPSSSLSALSSRAASVSSLHERILFAPGSEEAIERLKETEKIIAELNETW 451

Qy        456 EEKLAKTEEIHKEREAALEELGISIEK--GFVGPYHSKEMPHLVNLSDDPLLAECLVYNI 513
              |||| :|| |  |||| | |:|::: :  | :| :  |: ||||||::|||::|||:| |
Db        452 EEKLRRTEAIRMEREALLAEMGVAMREDGGTLGVFSPKKTPHLVNLNEDPLMSECLLYYI 511

Qy        514 KPGQTRVGNVNQDTQAEIRLNGSKILKEHCTFEN-----VDNVVTIVPNEKAAVMVNGVR 568
              | | ||||  : : : :| |:|  | :||| | :      : |||: | | |   ||| :
Db        512 KDGITRVGREDGERRQDIVLSGHFIKEEHCVFRSDSRGGSEAVVTLEPCEGADTYVNGKK 571

Qy        569 IDKPTRLRSGYRIILGDFHIFRFNHPEEARAERQEQSLLRHSVTNSQLGSPAPGRHDRTL 628
              : :|: |||| |||:|  |:||| |||:|| ||:
Db        572 VTEPSILRSGNRIIMGKSHVFRFTHPEQARQERER----------------------- 606

Qy        629 SKAGSDADGDSRSDSPLPHFRGKDSDWFYARREAASAILGLDQKISHLTDDELDALFDDV 688
                          :|      :  || :|:||      |:| |     :  |  | |
Db        607 --------------TPCAETPAEPVDWAFAQRELLEK-QGIDMK--QEMEQRLQELEDQY 649

Qy        689 QKARAVRRGLVEDNEDSDSQSSFPVRDKYMSN 720
              :: |     |:|  :  | :|      | | :
Db        650 RREREEATYLLE-QQRLDYESKLEALQKQMDS 680
```

RESULT 15
ABM83652
ID ABM83652 standard; protein; 1697 AA.
XX
AC ABM83652;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3901.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI; 2004-329368/30.
DR N-PSDB; ACN42304.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 1697 AA;

Query Match 41.2%; Score 1659.5; DB 8; Length 1697;
Best Local Similarity 46.7%; Pred. No. 5.2e-117;
Matches 350; Conservative 126; Mismatches 167; Indels 107; Gaps 15;

```
Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||: | :|||::| |: | :  |   :|            ||:|:
Db          3 GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET----------PKSFS 51

Qy         64 FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
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```
Db         52 FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG 109

Qy        121 YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178

Db        110 KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV 168

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238

Db        169 REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK 228

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298

Db        229 RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM 288

Qy        299 ---SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADS 355

Db        289 XPPQNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADR 348

Qy        356 AKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGAGGSGGPVEESYPPDTPL 415

Db        349 AKQIRCNAVINEDPNNKLIRELKDEVTRLRDLLYAQGLG---------------DITDM 392

Qy        416 EKQIVSIQQPDATVKKMS-----------------KAEIVEQLNQSEKLYRDLNQTWEE 457

Db        393 TNALVGM-SPSSSLSALSSRAASVSSLHERILFAPGSEEAIERLKETEKIIAELNETWEE 451

Qy        458 KLAKTEEIHKEREAALEELGISIEK--GFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKP 515

Db        452 KLRRTEAIRMEREALLAEMGVAMREDGGTLGVFSPKKTPHLVNLNEDPLMSECLLYYIKD 511

Qy        516 GQTRVGNVNQDTQAEIRLNGSKILKEHCTFEN-----VDNVVTIVPNEKAAVMVNGVRID 570

Db        512 GITRVGREDGERRQDIVLSGHFIKEEHCVFRSDSRGGSEAVVTLEPCEGADTYVNGKKVT 571

Qy        571 KPTRLRSGYRIILGDFHIFRFNHPEEARAERQEQSLLRHSVTNSQLGSPAPGRHDRTLSK 630

Db        572 EPSILRSGNRIIMGKSHVFRFNHPEQARQERER-------------------------- 604

Qy        631 AGSDADGDSRSDSPLPHFRGKDSDWFYARREAASAILGLDQKISHLTDDELDALFDDVQK 690

Db        605 -----------TPCAETPAEPVDWAFAQRELLEK-QGIDMK--QEMEQRLQELEDQYRR 649

Qy        691 ARAVRRGLVEDNEDSDSQSSFPVRDKYMSN 720

Db        650 EREEATYLLE-QQRLDYESKLEALQKQMDS 678


Search completed: September 1, 2006, 14:27:10
Job time : 194.583 secs
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: September 1, 2006, 14:22:42 ; Search time 263.166 Seconds
(without alignments)
2755.725 Million cell updates/sec

Title: US-09-235-416-1
Perfect score: 4030
Sequence: 1 MSGGGNIKVVVRVRPFNARE.....ELRQQQAQMEEALKTAKQEF 784

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3966	98.4	786	2	Q6IUU6_THELA	Q6iuu6 thermomyces
2	3216	79.8	1632	2	Q4X048_ASPFU	Q4x048 aspergillus
3	3168	78.6	1630	2	Q5AVY3_EMENI	Q5avy3 aspergillus
4	2842	70.5	1962	2	Q7S784_NEUCR	Q7s784 neurospora
5	2814.5	69.8	1087	2	Q86Z92_GIBMO	Q86z92 gibberella
6	2773	68.8	1814	2	Q86ZB4_BOTCI	Q86zb4 botrytis ci
7	2761.5	68.5	1793	2	Q4HXW9_GIBZE	Q4hxw9 gibberella
8	2721	67.5	1666	2	Q86ZA3_COCHE	Q86za3 cochliobolu
9	2634	65.4	1519	2	Q2UE08_ASPOR	Q2ue08 aspergillus
10	1957.5	48.6	1676	2	Q4P0W2_USTMA	Q4p0w2 ustilago ma
11	1957.5	48.6	1676	2	Q8TG36_USTMA	Q8tg36 ustilago ma
12	1932.5	48.0	1556	2	Q55Z46_CRYNE	Q55z46 cryptococcu
13	1895	47.0	1556	2	Q5KNG1_CRYNE	Q5kng1 cryptococcu
14	1691	42.0	1153	2	Q4VXC3_HUMAN	Q4vxc3 homo sapien
15	1683.5	41.8	1797	2	Q4R9M8_HUMAN	Q4r9m8 homo sapien
16	1680.5	41.7	1770	2	Q4VXC5_HUMAN	Q4vxc5 homo sapien
17	1677	41.6	1161	2	Q8JIX1_BRARE	Q8jix1 brachydanio
18	1676.5	41.6	1783	2	Q4R9M7_HUMAN	Q4r9m7 homo sapien
19	1673.5	41.5	1809	2	Q4R9M9_HUMAN	Q4r9m9 homo sapien
20	1673	41.5	1478	2	Q4LE42_HUMAN	Q4le42 homo sapien
21	1672	41.5	1698	2	Q6TA13_MOUSE	Q6ta13 mus musculu
22	1670	41.4	1679	2	Q7PHR1_ANOGA	Q7phr1 anopheles g
23	1669.5	41.4	1690	2	Q53T78_HUMAN	Q53t78 homo sapien
24	1669.5	41.4	1690	2	Q2NKJ6_HUMAN	Q2nkj6 homo sapien
25	1669.5	41.4	1816	1	KIF1B_HUMAN	O60333 homo sapien
26	1669	41.4	937	2	Q5SX63_MOUSE	Q5sx63 mus musculu
27	1669	41.4	1100	1	KIF1C_MOUSE	O35071 mus musculu
28	1668.5	41.4	1689	2	Q6P5H4_MOUSE	Q6p5h4 mus musculu
29	1668.5	41.4	1698	2	Q3UH16_MOUSE	Q3uh16 mus musculu
30	1668.5	41.4	1816	2	Q4VXC6_HUMAN	Q4vxc6 homo sapien
31	1668.5	41.4	1823	2	Q4VXC4_HUMAN	Q4vxc4 homo sapien
32	1667.5	41.4	1816	1	KIF1B_RAT	O88658 rattus norv
33	1667	41.4	1103	1	KIF1C_HUMAN	O43896 homo sapien
34	1667	41.4	1120	2	Q6A011_MOUSE	Q6a011 mus musculu
35	1665	41.3	1103	2	Q5U618_HUMAN	Q5u618 homo sapien
36	1663.5	41.3	1690	1	KIF1A_HUMAN	Q12756 homo sapien
37	1663.5	41.3	1695	1	KIF1A_MOUSE	P33173 mus musculu
38	1660.5	41.2	1816	1	KIF1B_MOUSE	Q60575 mus musculu
39	1659	41.2	1100	2	Q8VI89_MOUSE	Q8vi89 mus musculu
40	1657.5	41.1	628	2	Q3UY61_MOUSE	Q3uy61 mus musculu
41	1630.5	40.5	1671	2	Q9NBL1_DROME	Q9nbl1 drosophila
42	1629	40.4	1670	2	Q8MLF6_DROME	Q8mlf6 drosophila
43	1617	40.1	1097	1	KIF1C_RAT	O35787 rattus norv
44	1611	40.0	1576	2	Q61GI3_CAEBR	Q61gi3 caenorhabdi
45	1590.5	39.5	1584	1	UN104_CAEEL	P23678 caenorhabdi

ALIGNMENTS

RESULT 1
Q6IUU6_THELA
ID Q6IUU6_THELA PRELIMINARY; PRT; 786 AA.
AC Q6IUU6;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Unc104/KIF1A-like protein (Fragment).
OS Thermomyces lanuginosus (Humicola lanuginosa).
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Thermomyces.
OX NCBI_TaxID=5541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Rivera S.B., Koch S.J., Bauer J.M., Edwards J.M., Bachand G.D.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
CC ---
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC ---
DR EMBL; AY623608; AAT39887.1; -; mRNA.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR000253; FHA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00498; FHA; 1.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISc; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
FT NON_TER 786 786
SQ SEQUENCE 786 AA; 87201 MW; A008023FBAA70E12 CRC64;

Query Match 98.4%; Score 3966; DB 2; Length 786;
Best Local Similarity 98.9%; Pred. No. 4.6e-194;
Matches 775; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

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Qy          1 MSGGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSGGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPK 60

Qy         61 AFAFDRSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AFAFDRSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120

Qy        121 YGKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YGKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
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Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240

Qy        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS 300

Qy        301 GKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKRIK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKRIK 360

Qy        361 NHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGAGGSGGPVEESYPPDTPLEKQIV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGAGGSGGPVEESYPPDTPLEKQIV 420

Qy        421 SIQQPDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISI 480
              ||:||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SIRQPDGTVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISI 480

Qy        481 EKGFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKILK 540
              ||||||    |:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EKGFVGLTTPKKMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKILK 540

Qy        541 EHCTFENVDNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHPEEARAE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 EHCTFENVDNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHPEEARAE 600

Qy        601 RQEQSLLRHSVTNSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHFRGKDSDWFYARR 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RQEQSLLRHSVTNSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHFRGKDSDWFYARR 660

Qy        661 EAASAILGLDQKISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDSQSSFPVRDKYMSN 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 EAASAILGLDQKISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDSQSSFPVRDKYMSN 720

Qy        721 GTIDNFSLDTAITMPGTPRSDDDGDALFFGDKKSKQDASNVDVEELRQQQAQMEEALKTA 780
              |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        721 GTIDNFSLDTAITMPGTPRSDDDGDALKKGDKKSKQDASNVDVEELRQQQAQMEEALKTA 780

Qy        781 KQEF 784
              ||||
Db        781 KQEF 784
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RESULT 2
Q4X048_ASPFU
ID   Q4X048_ASPFU   PRELIMINARY;   PRT;  1632 AA.
AC   Q4X048;
DT   05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2005, sequence version 1.
DT   07-MAR-2006, entry version 6.
DE   Kinesin family protein.
GN   ORFNames=Afu2g14730;
OS   Aspergillus fumigatus (Sartorya fumigata).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX   NCBI_TaxID=5085;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Af293 / CBS 101355 / FGSC A1100;
RX   PubMed=16372009; DOI=10.1038/nature04332;
RA   Nierman W.C., Pain A., Anderson M.J., Wortman J.R., Kim H.S.,
RA   Arroyo J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.W.,
RA   Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,
RA   Farman M., Fedorova N., Fedorova N.D., Feldblyum T.V., Fischer R.,
RA   Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA   Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.J.,
RA   Haas H., Harris D.E., Horiuchi H., Huang J., Humphray S., Jimenez J.,
RA   Keller N., Khouri H., Kitamoto K., Kobayashi T., Konzack S.,
RA   Kulkarni R., Kumagai T., Lafton A., Latge J.-P., Li W., Lord A.,
RA   Lu C., Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M.,
RA   Monod M., Mouyna I., Mulligan S., Murphy L.D., O'Neil S., Paulsen I.,
RA   Penalva M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,
RA   Rabbinowitsch E., Rawlins N., Rajandream M.A., Reichard U.,
RA   Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA   Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA   Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA   Takeuchi M., Tekaia F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA   White O., Woodward J.R., Yu J.-H., Fraser C.M., Galagan J.E., Asai K.,
RA   Machida M., Hall N., Barrell B.G., Denning D.W.;
RT   "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT   Aspergillus fumigatus.";
RL   Nature 438:1151-1156(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AAHF01000001; EAL93767.1; -; Genomic_DNA.
DR   GO; GO:0005875; C:microtubule associated complex; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003777; F:microtubule motor activity; IEA.
DR   GO; GO:0007018; P:microtubule-based movement; IEA.
DR   InterPro; IPR001752; kinesin_motor.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR011993; PH_type.
DR   Pfam; PF00498; FHA; 1.
DR   Pfam; PF00225; Kinesin; 1.
DR   Pfam; PF00169; PH; 1.
DR   PRINTS; PR00380; KINESINHEAVY.
DR   SMART; SM00129; KISc; 1.
DR   SMART; SM00233; PH; 1.
DR   PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR   PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
KW   Complete proteome.
SQ   SEQUENCE   1632 AA;  182726 MW;  1CAED6825E77444D CRC64;
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  Best Local Similarity   78.6%;  Pred. No. 2.5e-155;
  Matches  636;  Conservative   68;  Mismatches   73;  Indels   32;  Gaps    8;

Qy          3 GGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKS-GKTIMDGPKA 61
              |||||||||||||||:|||||||||||:|:|||||| |||||:||:||: ||  ::|||
Db          5 GGGNIKVVVRVRPFNSREIDRGAKCIVQMKGNQTILVPPPGADEKSRKAGGKGAVEGPKT 64

Qy         62 FAFDRSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGY 121
              |||||||||||||||| |::|| |||||||||:|||||||||||||||||||||||||||
Db         65 FAFDRSYWSFDKNAPNYAGQDNLFADLGVPLLDNAFQGYNNCIFAYGQTGSGKSYSMMGY 124

Qy        122 GKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVREH 181
              |||:||||||||:||:|| ::|:|||| |||||||||||||||||||| |||||||||
Db        125 GKEYGVIPRICQEMFQRIAKMQEDKNLNCTVEVSYLEIYNERVRDLLNPSNKGNLKVREH 184

Qy        182 PSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWHD 241
              |||||||||||||| ||||:||::|||||||||||||||||||||||||||||||||| ||
Db        185 PSTGPYVEDLAKLAVRSFEEIDHLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKRHD 244

Qy        242 EETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSSG 301
              || ||||||::|||||||||||| ||||||||||||||||||||||||||||::||
Db        245 AETSMDTEKVSRISLVDLAGSERANSTGATGARLKEGAEINRSLSTLGRVIAALADVASG 304

Qy        302 KQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKRIKN 361
              |:|   :||||||:||||||||||||||||||||||||:|||||||||||||||||
Db        305 KKKNASMVPYRDSILTWLLKDSLGGNSMTAMIAAISPADINFDETLSTLRYADSAKRIKN 364

Qy        362 HAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGAGGSGG-PVEESYPPDTPLEKQIV 420
              ||||||||||||||||||||:||    |||  || :|| | || ||||||||||:|
Db        365 HAVVNEDPNARMIRELKEELAQLRAKL----GGGSTAGAAGGMPAEEYYPPDTPLEKQMV 420

Qy        421 SIQQPDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISI 480
              |||: | |: |:|||||||||||||:|||||||||| ||| ||:|||||||||||||
Db        421 SIQKADGTITKVSKAEIVEQLNQSEKLYKDLNQTWEEKLEKTERIHREREAALEELGISI 480
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Qy        481 EKGFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKILK 540
Db        481 EKGFVGLSTPKKMPHLVNLSDDPLLAECLVYNIKPGTTTVGNMEQGSHVEIRLNGSKILP 540

Qy        541 EHCTFENVDNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHPEEARAE 600
Db        541 NHCTFENVDNVVTIVPSEGAAVMVNGLRIDKPKRLKSGFRIILGDFHIFRFNHPQEARAE 600

Qy        601 RQEQSLLRHSVTNSQLGSPAPGR-HDRTLSKAGSDADGD-SRSDSPLPHFRGKDSDWFYA 658
Db        601 RVEQSLLRHSVTTSQLGSPAPTKTHDRTMSKTGSELDGDSSRADSPMQAQRGGEADWFYA 660

Qy        659 RREAASAILGLDQKISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDSQSSFPVRDKYM 718
Db        661 RREAVSAILGPDH-ISHMPDDELDALFEDVQKVRATRRGLVENEDDSDSLSSFPVRDKYM 719

Qy        719 SNGTIDNFSLDTAITMPGTPRSDDDGDALFFGD---KKSKQD---------------- 757
Db        720 SNGTIDNFSLDTAITMPGTPGQQYDGEGQNGSDFTLQAARQDMQRHLDKQKEEFKNKLRI 779

Qy        758 --ASNVDVEELRQQQAQMEEALKTAKQEF 784
Db        780 AEASDQDADELRLEKERMEEALRSTKEEY 808


RESULT 3
Q5AVY3_EMENI
ID   Q5AVY3_EMENI    PRELIMINARY;    PRT;  1630 AA.
AC   Q5AVY3;
DT   26-APR-2005, integrated into UniProtKB/TrEMBL.
DT   26-APR-2005, sequence version 1.
DT   07-MAR-2006, entry version 9.
DE   Hypothetical protein.
GN   ORFNames=AN7547.2;
OS   Aspergillus nidulans FGSC A4.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; Emericella.
OX   NCBI_TaxID=227321;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=FGSC 4;
RX   PubMed=16372000; DOI=10.1038/nature04341;
RA   Galagan J.E., Calvo S.E., Cuomo C., Ma L.-J., Wortman J.R.,
RA   Batzoglou S., Lee S.-I., Bastuerkmen M., Spevak C.C., Clutterbuck J.,
RA   Kapitonov V., Jurka J., Scazzocchio C., Farman M., Butler J.,
RA   Purcell S., Harris S., Braus G.H., Draht O., Busch S., D'Enfert C.,
RA   Bouchier C., Goldman G.H., Bell-Pedersen D., Griffiths-Jones S.,
RA   Doonan J.H., Yu J., Vienken K., Pain A., Freitag M., Selker E.U.,
RA   Archer D.B., Penalva M.A., Oakley B.R., Momany M., Tanaka T.,
RA   Kumagai T., Asai K., Machida M., Nierman W.C., Denning D.W.,
RA   Caddick M., Hynes M., Paoletti M., Fischer R., Miller B.L., Dyer P.S.,
RA   Sachs M.S., Osmani S.A., Birren B.W.;
RT   "Sequencing of Aspergillus nidulans and comparative analysis with A.
RT   fumigatus and A. oryzae.";
RL   Nature 438:1105-1115(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AACD01000129; EAA62127.1; -; Genomic_DNA.
DR   GO; GO:0005875; C:microtubule associated complex; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003777; F:microtubule motor activity; IEA.
DR   GO; GO:0007018; P:microtubule-based movement; IEA.
DR   InterPro; IPR000253; FHA.
DR   InterPro; IPR001752; kinesin_motor.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR011993; PH_type.
DR   Pfam; PF00498; FHA; 1.
DR   Pfam; PF00225; Kinesin; 1.
DR   Pfam; PF00169; PH; 1.
DR   PRINTS; PR00380; KINESINHEAVY.
DR   SMART; SM00129; KISc; 1.
DR   SMART; SM00233; PH; 1.
DR   PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR   PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   1630 AA;  182784 MW;  85AD0AF238645F9D CRC64;

  Query Match             78.6%;  Score 3168;  DB 2;  Length 1630;
  Best Local Similarity   78.0%;  Pred. No. 7.1e-153;
  Matches  627;  Conservative   73;  Mismatches   78;  Indels   26;  Gaps   10;

Qy          3 GGGNIKVVVRVRPFNARE-IDRGAKCIVRMEGNQTILTPPPGAEEKARKSG-KTIMDGPKA 61
Db          5 GGGNIKVVVRVRPFNSREIERGAKCIVQMKDSQTILTPPPGAEEKSRKGGNKAAAEGPKT 64

Qy         62 FAFDRSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGY 121
Db         65 FAFDRSYWSFDKKAPNYAGQDNLFSDLGVPLLDNAFQGYNNCIFAYGQTGSGKSYSMMGY 124

Qy        122 GKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVREH 181
Db        125 GKEYGVIPRICQDMFERIRKIQEDKNLTCTVEVSYLEIYNERVRDLLNPSNKGNLKVREH 184

Qy        182 PSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWHD 241
Db        185 PSTGPYVEDLAKLAVRSFEEIENLMDEGNKARTVAATNMNETSSRSHAVFTLMLTQKRHD 244

Qy        242 EETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSSG 301
Db        245 AETSMDTEKVSRISLVDLAGSERANSTGATGARLKEGAEINRSLSTLGRVIAALADAASG 304

Qy        302 KQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKRIKN 361
Db        305 K-KKGKQVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFDETLSTLRYADSAKRIKN 363

Qy        362 HAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGAGGSGGPV-EESYPPDTPLEKQIV 420
Db        364 HAVVNEDPNARMIRELKDELAQLRAKLGGGAAGGATAGAAGGVVADEVYPPDTPMEKQMV 423

Qy        421 SIQQPDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISI 480
Db        424 SIQQPDGTIKKVSKAEIVEQLNQSEKLYKDLNQTWEEKLIKTEQIHKEREAALEELGISI 483

Qy        481 EKGFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKILK 540
Db        484 EKGFIGLSTPKKMPHLVNLSDDPLLAECLVYNLKPGVTHVGNMDQGNHVEIRLNGSKILA 543

Qy        541 EHCTFENVDNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHPEEARAE 600
Db        544 DHCKFENVDNVVTILPSEGAAVMVNGVRVDKPKRLKSGYRIILGDFHIFRFNHPQEARAE 603

Qy        601 RQEQSLLRHSVTNSQLGSPAPGR-HDRTLSKAGSDADGD-SRSDSPLPHFRGKDSDWFYA 658
Db        604 RVEQSLLRHSVTTSQLASPAPGKAHERNVSKA-SDLDWDSSRADSPMGFQRGRESDWFYA 662

Qy        659 RREAASAILGLD-QKISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDSQSSFPVRDKY 717
Db        663 RREAVSA--GMDPDRLAHMPDDELDALFENVQNVRANRRGLLENEEDSDSLSSYPIRDKY 720

Qy        718 MSNGTIDNFSLDTAITMPGTPRSDDDGDAL----------------FFGDKKSKQDAS-N 760
Db        721 MSNGTIDNFSLDTAITMPGTPRHGDEDATLQSVRQDMQRQLERQKEQYLDKLRESEASPS 780

Qy        761 VDVEELRQQQAQMEEALKTAKQEF 784
Db        781 QGIDELRSEKARMEDALRVAKEEY 804


RESULT 4
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Q7S784_NEUCR
ID   Q7S784_NEUCR   PRELIMINARY;   PRT;  1962 AA.
AC   Q7S784;
DT   15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT   15-DEC-2003, sequence version 1.
DT   07-FEB-2006, entry version 15.
DE   Hypothetical protein.
GN   ORFNames=NCU06733.1;
OS   Neurospora crassa.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX   NCBI_TaxID=5141;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=74-OR23-1A / FGSC 987;
RX   MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;
RA   Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA   Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA   Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA   Qui D., Ianakiev P., Bell-Pedersen D., Nelson M.A.,
RA   Werner-Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L.,
RA   Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,
RA   Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
RA   Stange-Thomann N., Barrett R., Gnerre S., Kamal M., Kamvysselis M.,
RA   Mauceli E., Bielke C., Rudd S., Frishman D., Krystofova S.,
RA   Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C.,
RA   Macino G., Catcheside D.E.A., Li W., Pratt R.J., Osmani S.A.,
RA   DeSouza C.P.C., Glass N.L., Orbach M.J., Berglund J.A., Voelker R.,
RA   Yarden O., Plamann M., Seiler S., Dunlap J.C., Radford A., Aramayo R.,
RA   Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA   Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.W.;
RT   "The genome sequence of the filamentous fungus Neurospora crassa.";
RL   Nature 422:859-868(2003).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AABX01000301; EAA31425.1; -; Genomic_DNA.
DR   HSSP; P33173; 1I5S.
DR   GO; GO:0005875; C:microtubule associated complex; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003777; F:microtubule motor activity; IEA.
DR   GO; GO:0007018; P:microtubule-based movement; IEA.
DR   InterPro; IPR000253; FHA.
DR   InterPro; IPR001752; kinesin_motor.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR011993; PH_type.
DR   Pfam; PF00498; FHA; 1.
DR   Pfam; PF00225; Kinesin; 1.
DR   Pfam; PF00169; PH; 1.
DR   PRINTS; PR00380; KINESINHEAVY.
DR   SMART; SM00240; FHA; 1.
DR   SMART; SM00129; KISc; 1.
DR   SMART; SM00233; PH; 1.
DR   PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR   PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   1962 AA;  214863 MW;  180ADBB5E87834D4 CRC64;

  Query Match             70.5%;  Score 2842;  DB 2;  Length 1962;
  Best Local Similarity   71.2%;  Pred. No. 4.1e-136;
  Matches  581;  Conservative   71;  Mismatches  118;  Indels   46;  Gaps   11;

Qy          1 MSGGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPK 60
              | |||||||||| |||||||  ||||:||| |  |||:|| || |  |  |       | |
Db          8 MGGGGNIKVVVRCRPFNAREHDRGAQCIVEMRDNQTVLTTPPDAVVKGGKD-----QGQK 62

Qy         61 AFAFDRSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
              |||||||||||||||||  |: | :||| |||||||:|||||||||||||||||||||||
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Db         63 IFAFDRSYWSFDKNAPNYAGQDQLHEDLGKPLLDNAFQGYNNCIFAYGQTGSGKSYSMMG 122

Qy        121 YGKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
              |||: |:|| ||||||:|||::|:|||| ||||||||||||||||||||: ||||||||
Db        123 YGKDAGIIPMICQDMFKRINDMQQDKNLRCTVEVSYLEIYNERVRDLLNPANKGNLKVRE 182

Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240
              |||||||||||||||| ||||||:|||||||||||||||||||||||||||||| ||||
Db        183 HPSTGPYVEDLAKLVVGSFQEIEHLMDEGNKARTVAATNMNETSSRSHAVFTLMLTQKRF 242

Qy        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS 300
              | ||||: || ||||||||||||||||||||||||||||||||||||||||||||||:|:
Db        243 DPETKMEMEKAAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADLST 302

Qy        301 GKQKKNQL---VPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK 357
              ||:||      |||||||||||||||||||||||||||||::||||||||||||||
Db        303 GKKKKGSAAGQVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINYDETLSTLRYADSAK 362

Qy        358 RIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGAGGSGGPVEESYPPDTPLEK 417
              |||||||||| |||||||||||||||||     | ||  | :  | || |   |||||
Db        363 RIKNHAVVNEDANARMIRELKEELAQLRSKL----GNGGVVGDTHVPGEEVYAEGTPLEK 418

Qy        418 QIVSIQQPDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELG 477
              |||||  || ||||:||||| |||||||| :|||||||:|| ||||||||||||||||
Db        419 QIVSITTPDGTVKKVSKAEIAEQLNQSEKLLQDLNQTWEQKLQKTEEIHKEREAALEELG 478

Qy        478 ISIEKGFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNV--NQDTQAEIRLNG 535
              |||||||:|    |:|||||||||||||||||:||| | ||||  | : || |||||
Db        479 ISIEKGFIGMSTPKKMPHLVNLSDDPLLAECLVYNLKPGSTSVGNVESNAEHQANIRLNG 538

Qy        536 SKILKEHCTFEN-VDNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHP 594
              |:|| ||| ||| |  ||::| | ||||||| |: :|||| ||||||||||||||||||
Db        539 SRILHEHCVFENAADGTVTVIPKEGAAVMVNGKRVTEPTRLHSGYRIILGDFHIFRFNHP 598

Qy        595 EEARAER----QEQSLLRHSVTNSQLG--------SPAPGRHDRTLSKAGSDADGDSRSD 642
               ||:|||    ::||||| |:| :||         ||:   | ::|| | |: |  || |
Db        599 LEAKAERAERAEQQSLLRQSLTANQLQALEKSPNLSPS-HNHQQSLSTAVSEGD-SSRPD 656

Qy        643 SPLPHFRG-KDSDWFYARREAASAILGLDQKISHLTDDELDALFDDVQKARAVRRGLVED 701
              || |  |  |:||| :|||||| |||| ||  : |||:||:|||:|||:||| |  : |
Db        657 SPAPFSRNTKESDWSFARREAAGAILGTDQNFAKLTDEELNALFEDVQRARAERVNVREG 716

Qy        702 NEDSDSQSSFPVRDKYMSNGTIDNFSLDTAITMPGTPRSDDDGDAL---------------- 747
              :|| :| :|:| |:||:| ||:|||||||:||| ||:  :  : |
Db        717 DEDIESMASYPTREKYLSTGTLDNFSLDTALTMPSTPKQAETEEKLGQIRDVMQGQLDKQ 776

Qy        748 --FFGDKKSKQDASNVDVEELRQQQAQMEEALKTAK 781
                 : |:    :|:||:|||:::::|:||| |   |
Db        777 KEEYKDQLKTAEAANVEVEEIKKEKARMEETLMQLK 812


RESULT 5
Q86Z92_GIBMO
ID   Q86Z92_GIBMO   PRELIMINARY;   PRT;  1087 AA.
AC   Q86Z92;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 16.
DE   Kinesin.
GN   Name=KLP8;
OS   Gibberella moniliformis (Fusarium verticillioides).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX   NCBI_TaxID=117187;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22627967; PubMed=12742059; DOI=10.1016/S1087-1845(03)00022-7;
RA   Schoch C.L., Aist J.R., Yoder O.C., Gillian Turgeon B.;
RT   "A complete inventory of fungal kinesins in representative filamentous
RT   ascomycetes.";
RL   Fungal Genet. Biol. 39:1-15(2003).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; AY230444; AAO59306.1; -; Genomic_DNA.
DR   HSSP; P33173; 1I5S.
DR   GO; GO:0005874; C:microtubule; IEA.
DR   GO; GO:0005875; C:microtubule associated complex; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003777; F:microtubule motor activity; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0007018; P:microtubule-based movement; IEA.
DR   InterPro; IPR000253; FHA.
DR   InterPro; IPR001752; kinesin_motor.
DR   Pfam; PF00498; FHA; 1.
DR   Pfam; PF00225; Kinesin; 1.
DR   PRINTS; PR00380; KINESINHEAVY.
DR   SMART; SM00129; KISc; 1.
DR   PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR   PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW   ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ   SEQUENCE   1087 AA;  120899 MW;  BB7F19ADB309C4D5 CRC64;

  Query Match           69.8%;  Score 2814.5;  DB 2;  Length 1087;
  Best Local Similarity  70.3%;  Pred. No. 4.6e-135;
  Matches  575;  Conservative   82;  Mismatches  112;  Indels   49;  Gaps   14;

Qy          2 SGGGNIKVVVRVRPFNARE IDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKA 61
              :|||||||||| ||||:|||:|||||| |:||||::| | |   |  | |     ||||
Db          4 TGGGNIKVVVRCRPFNSRE IERGAKCIVEMKGNQTVVTAPEG---KGVKDG-----GPKA 55

Qy         62 FAFDRSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGY 121
              ||||||||||:|: |||| | :|| ||| |||||||:|||||||||||||||||||||||
Db         56 FAFDRSYWSFNKDDPNYAGQSNLFDDLGQPLLDNAFQGYNNCIFAYGQTGSGKSYSMMGY 115

Qy        122 GKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVREH 181
              ||| |::| |||||||||:||:|||   |||||||||||||||||||||||||||||||| 
Db        116 GKEIGIVPLICQDMFRRIDELKKDKTTKCTVEVSYLEIYNERVRDLLNPSTKGNLKVREH 175

Qy        182 PSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWHD 241
              |||||||||||| |  |||||:||||||||||||||:|||||||||| |||| :|
Db        176 PSTGPYVEDLAKLAVNEFQEIEHLMDEGNKARTVAATNMNQTSSRSHAVFTLMLTQKKYD 235

Qy        242 EETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSSG 301
              :|||: |||||||||||||||||||||||||||||||||||||||||||||||:|:|
Db        236 ADTKMEMEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADLSTG 295

Qy        302 KQKKNQL--VPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKRI 359
              :||     |||||||||||||||||||||||||||:|||||||:|||||||||||||||
Db        296 GKKKKGTGQVPYRDSVLTWLLKDSLGGNSMTAMIAAVSPADINFDETLSTLRYADSAKRI 355

Qy        360 KNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGAGGSGGPVEESYPPDTPLEKQI 419
              |||||||| |||||||||||: |||||  :|   ||| | |    |:||  |||::|:
Db        356 KNHAVVNEDANARMIRELKEELSLLRSKL-GNGPVPGGAAGGGLVTGETYPEGTPLDQQM 414

Qy        420 VSIQQPDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGIS 479
              |||    |  :||:|||| |||:|||||  |||||||||| ||||||||||||||||:|
Db        415 VSITGSDGVLKKVSKAEIAEQLSQSEKLLTDLNQTWEEKLLKTEEIHKEREAALEELGVS 474

Qy        480 IEKGFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNV--NQDTQAEIRLNGSK 537
              ||||||| :  |:|||||||||||||||||:||| | ||||   | | || ||||||:
Db        475 IEKGFVGLHTPKKMPHLVNLSDDPLLAECLVYNLKPGTTTVGNVDTNADHQANIRLNGSR 534

Qy        538 ILKEHCTFENV-DNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHPEE 596
              || :|||||  |  ||: |:| |:||:|| || :|::| ||||:||||||||||||| |
Db        535 ILHDHCTFENAPDGTVTLTPSEGASVMINGKRITEPSQLHSGYRVILGDFHIFRFNHPME 594

Qy        597 ARAERQE-----QSLLRHSVTNSQL-----GSPAPG---RHDRTLSKAGSDADGDSRSDS 643
              ||||| |     |||||||:| |||     |||:|     |:|: |:      |  || :|
Db        595 ARAERAEVPERPQSLLRHSITASQLQALDRGSPSPSPRPGHERSFSRVSEFGD-ISRPES 653

Qy        644 PLPHFR-GKDSDWFYARREAASAILGLDQKISHLTDDELDALFDDVQKARAVRRGLVEDN 702
              |    | |::|||  |||||| |||| || :: |||:||:|||:|||:||| |   |
Db        654 PSIFQRSGRESDWSLARREAAGAILGSDQNLTSLTDEELNALFEDVQRARAER---VNGR 710

Qy        703 ED-SDSQSSFPVRDKYMSNGTIDNFSLDTAITMPGTPRSDDDGDAL---------- 747
              ||  ||:||:|:||||:||||:||||||||:||| ||:  :  | |
Db        711 EDGDDSESSYPIRDKYLSNGTMDNFSLDTALTMPSTPKQGEPDDRLKEVREELQNRLEKQ 770

Qy        748 --FFGDKKSKQDASNVDVEELRQQQAQMEEALKTAKQE 783
                : |:    :|:||::||::|:: :|| |||  |::
Db        771 KEEYQDQLKSAEAANVEIEEIKQEKVKMEAALKELKED 808


RESULT 6
Q86ZB4_BOTCI
ID   Q86ZB4_BOTCI   PRELIMINARY;   PRT;  1814 AA.
AC   Q86ZB4;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 17.
DE   Kinesin.
GN   Name=KLP8;
OS   Botrytis cinerea (Noble rot fungus) (Botryotinia fuckeliana).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
OC   Helotiales; Sclerotiniaceae; Botryotinia.
OX   NCBI_TaxID=40559;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22627967; PubMed=12742059; DOI=10.1016/S1087-1845(03)00022-7;
RA   Schoch C.L., Aist J.R., Yoder O.C., Gillian Turgeon B.;
RT   "A complete inventory of fungal kinesins in representative filamentous
RT   ascomycetes.";
RL   Fungal Genet. Biol. 39:1-15(2003).
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; AY230422; AAO59284.1; -; Genomic_DNA.
DR   HSSP; P33173; 1I5S.
DR   GO; GO:0005875; C:microtubule associated complex; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003777; F:microtubule motor activity; IEA.
DR   GO; GO:0007018; P:microtubule-based movement; IEA.
DR   InterPro; IPR000253; FHA.
DR   InterPro; IPR001752; kinesin_motor.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR011993; PH_type.
DR   Pfam; PF00498; FHA; 1.
DR   Pfam; PF00225; Kinesin; 1.
DR   Pfam; PF00169; PH; 1.
DR   PRINTS; PR00380; KINESINHEAVY.
DR   SMART; SM00129; KISc; 1.
DR   SMART; SM00233; PH; 1.
DR   PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR   PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
SQ   SEQUENCE   1814 AA;  201181 MW;  5F989F1BF2622BA1 CRC64;

  Query Match           68.8%;  Score 2773;  DB 2;  Length 1814;
  Best Local Similarity  72.7%;  Pred. No. 1.2e-132;
  Matches  575;  Conservative   63;  Mismatches  105;  Indels   48;  Gaps   14;

Qy         31 MEGNQTILTPPPGAEEKAR--KSGKTIMDGPKAFAFDRSYWSFDKNAPNYARQEDLFQDL 88
              |:  ||::||| | | |:|  | ||    | | ||||||||||||| |:|| |::|  ||
Db          1 MKDAQTVITPPEGHEAKSRDAKGGKA-DTGQKVFAFDRSYWSFDKNDPSYAGQDNLHTDL 59

Qy         89 GVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYGKEHGVIPRICQDMFRRINELQKDKNL 148
              | |||||||:|||||||||||||||||||||||: ||||:|||||| || |||:||:|
Db         60 GKPLLDNAFQGYNNCIFAYGQTGSGKSYSMMGYGKDAGVIPKICQDMFERIGELQQDKHL 119

Qy        149 TCTVEVSYLEIYNERVRDLLNPSTKGNLKVREHPSTGPYVEDLAKLVVRSFQEIENLMDE 208
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        120 KCTVEVSYLEIYNERVRDLLNPSTKGNLKVREHPSTGPYVEDLAKLVVSSFQEIENLMDE 179

Qy        209 GNKARTVAATNMNETSSRSHAVFTLTLTQKWHDEETKMDTEKVAKISLVDLAGSERATST 268
              |||||||||||||||||||||||||||| | ||||  |||||||||||||||| ||
Db        180 GNKARTVAATNMNETSSRSHAVFTLTLTQKRLDVETKMAMEKVAKISLVDLAGSERANST 239
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Qy        269 GATGARLKEGAEINRSLSTLGRVIAALADMSSGKQKK----NQLVPYRDSVLTWLLKDSL 324
              ||||||||||||||||||||||||||||:| ||:||    || ||||||||||||||||
Db        240 GATGARLKEGAEINRSLSTLGRVIAALADLSEGKKKKVGKGNQ-VPYRDSVLTWLLKDSL 298

Qy        325 GGNSMTAMIAAISPADINFEETLSTLRYADSAKRIKNHAVVNEDPNARMIRELKEELAQL 384
              |||||||||||||||||||:|||||||||||||||||||||||| ||||||||||||||
Db        299 GGNSMTAMIAAISPADINFDETLSTLRYADSAKRIKNHAVVNEDANARMIRELKEELAQL 358

Qy        385 RSKLQSSGGGGGGAGGSGGPVEESYPPDTPLEKQIVSIQQPDATVKKMSKAEIVEQLNQS 444
              | ||  :||||   |||  | :| |   ||||||:|:|   |  |||:||||| ||||||
Db        359 RGKL--TGGGGWRRGGS--PADEIYAEGTPLEKQMVTIVSSDGAVKKVSKAEITEQLNQS 414

Qy        445 EKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISIEKGFVGPYHSKEMPHLVNLSDDPL 504
              |||| |||||||||| |||||||||||||||||||||||| :  |:||||||||||||
Db        415 EKLYSDLNQTWEEKLQKTEEIHKEREAALEELGISIEKGFVGLHTPKKMPHLVNLSDDPL 474

Qy        505 LAECLVYNIKPGQTRVGNV--NQDTQAEIRLNGSKILKEHCTFENVDNVVTIVPNEKAAV 562
              ||||||||:||| | ||||  |    |||||||::|| ||||||||||||: | | |||
Db        475 LAECLVYNLKPGSTSVGNVDTNAAHAAEIRLNGTRILHEHCTFENVDNVVTLTPTEGAAV 534

Qy        563 MVNGVRIDKPTRLRSGYRIILGDFHIFRFNHPEEARAERQEQSLLRHSVTNSQL------ 616
              |||| |::|||||||:|:||||||||||:| |||||| |||||||||| :||
Db        535 MVNGQRVEKPTRLRSGFRVILGDFHIFRFNNPTEARAERAEQSLLRHSVTANQLENFKDW 594

Qy        617 ------GSPAPGRHDRTLSKAGSDA--DGDSRSDSPLPHFRGKDSDWFYARREAASAILG 668
                   :| |  |||| ||| ||   || ||:|||:|  ||  |||  |||||| ||||
Db        595 DKFSPSSTPRPA-HDRTFSKAISDLDFDGSSRADSPVPG-RGL-SDWSLARREAAGAILG 651

Qy        669 LDQKISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDSQSSFPVRDKYMSNGTIDNFSL 728
              ||||: |:|:||: ||:|||:||| |      :| || :|:|:|:||:||||:|||||
Db        652 TDQKIAGLSDEELNVLFEDVQRARA-ERATANLEDDLDSVTSYPMREKYLSNGTLDNFSL 710

Qy        729 DTAITMPGTPRSDDDGDAL----------------FFGDKKSKQDASNVDVEELRQQQAQ 772
              |||:||| ||:  :  | :                | ::      |||:|||::::: :
Db        711 DTALTMPSTPKQGEVEDRMREVKEEMQVQLEKQREEFQEQLEIAKTSNVEVEEIKKEKVR 770

Qy        773 MEEALKTAKQE 783
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Db        771 MEETLREVKEE 781
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RESULT 7
Q4HXW9_GIBZE
ID   Q4HXW9_GIBZE   PRELIMINARY;   PRT;  1793 AA.
AC   Q4HXW9;
DT   16-AUG-2005, integrated into UniProtKB/TrEMBL.
DT   16-AUG-2005, sequence version 1.
DT   07-FEB-2006, entry version 6.
DE   Hypothetical protein.
GN   ORFNames=FG10189.1;
OS   Gibberella zeae (Fusarium graminearum).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX   NCBI_TaxID=5518;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=PH-1 / NRRL 31084;
RA   Birren B.W., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA   Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
RA   Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA   Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
RA   Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA   Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D.,
RA   Galagan J.E., Gardyna S., Gnerre S., Graham L., Grand-Pierre N.,
RA   Hafez N., Hagopian D., Hagos B., Hall J., Horton L., Hulme W.,
RA   Iliev I., Jaffe D., Johnson R., Jones C., Kamal M., Kamat A.,
RA   Karatas A., Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G.,
RA   Lui A., Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J.,
RA   Manning J., Matthews C., Mauceli E., McCarthy M., Meldrim J.,
RA   Meneus L., Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C.,
RA   Nicol R., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P.,
RA   O'Neil D., Oliver J., Peterson K., Phunkhang P., Pierre N.,
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RA   Purcell S., Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C.,
RA   Rogov P., Roman J., Schauer S., Schupback R., Seaman S., Severy P.,
RA   Smirnov S., Smith C., Spencer B., Stange-Thomann N., Stojanovic N.,
RA   Stubbs M., Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA   Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA   Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA   Lander E.S.;
RT   "Fusarium graminearum genome sequence.";
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AACM01000424; EAA70032.1; -; Genomic_DNA.
DR   GO; GO:0005875; C:microtubule associated complex; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003777; F:microtubule motor activity; IEA.
DR   GO; GO:0007018; P:microtubule-based movement; IEA.
DR   InterPro; IPR001752; kinesin_motor.
DR   InterPro; IPR001849; PH.
DR   Pfam; PF00498; FHA; 1.
DR   Pfam; PF00225; Kinesin; 1.
DR   Pfam; PF00169; PH; 1.
DR   PRINTS; PR00380; KINESINHEAVY.
DR   SMART; SM00129; KISc; 1.
DR   SMART; SM00233; PH; 1.
DR   PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR   PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   1793 AA;  198597 MW;  44AF342FED904207 CRC64;
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Query Match 68.5%; Score 2761.5; DB 2; Length 1793;
Best Local Similarity 68.8%; Pred. No. 4.7e-132;
Matches 564; Conservative 91; Mismatches 108; Indels 57; Gaps 16;

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Qy          2 SGGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMD-GPK 60
              :|||||||||| ||||:|||:| |:||| |:||||::| |          || : | |||
Db          4 AGGGNIKVVVRCRPFNSREIERNAQCIVEMKGNQTVITAP---------EGKGVKDSGPK 54

Qy         61 AFAFDRSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
              ||||||||||:|: |||| | :|| ||| |||||||:|||||||||||||||||||||||
Db         55 AFAFDRSYWSFNKDDPNYAGQSNLFDDLGQPLLDNAFEGYNNCIFAYGQTGSGKSYSMMG 114

Qy        121 YGKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
              |||| |::| |||::|:| :|:|||    |||||||||||||||||||||||||||||||
Db        115 YGKEIGIVPMICQEIFKRADEIQKDGKTKCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 174

Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240
              |||||||||||||| | :|||||:||||||||||||||||:|||||||||| ||||
Db        175 HPSTGPYVEDLAKLAVNTFQEIEHLMDEGNKARTVAATNMNQTSSRSHAVFTLMLTQKKI 234

Qy        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS 300
              | :|||  |||||||||||||||| |||||||||||||||||||||||||||||:|:
Db        235 DTDTKMALEKVAKISLVDLAGSERANSTGATGARLKEGAEINRSLSTLGRVIAALADLST 294

Qy        301 -GKQKKNQ-LVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKR 358
               ||:||   ||||||||||||||||||||||:|||||||:||||||||||||||
Db        295 PGKKKKGSGQVPYRDSVLTWLLKDSLGGNSMTAMIAAVSPADINFDETLSTLRYADSAKR 354

Qy        359 IKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGAGGS--GGPVEESYPPDTPLE 416
              |||||||||| ||||||||||: || ||    ||||| ||:   |   |:|   |||:
Db        355 IKNHAVVNEDANARMIRELKEELSLLRGKL----GGGGGPGGAVVAG---ETYAEGTPLD 407

Qy        417 KQIVSIQQPDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEEL 476
              :|:||| ||  :||:||||| |||:|||||  |||||||||| ||||||||||||||||
Db        408 QQMVSITGPDGVLKKVSKAEIAEQLSQSEKLLTDLNQTWEEKLLKTEEIHKEREAALEEL 467

Qy        477 GISIEKGFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNV--NQDTQAEIRLN 534
              |:|||||||| :  |:|||||||||||||||||:||| | ||||  | | || ||||
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Db        468 GVSIEKGFVGLHTPKKMPHLVNLSDDPLLAECLVYNLKPGTTTVGNVDTNADHQANIRLN 527

Qy        535 GSKILKEHCTFEN-VDNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNH 593

Db        528 GSRILHDHCSFENAADGTVTLTPSEGASVMINGKRITEPSQLHSGYRVILGDFHIFRFNH 587

Qy        594 PEEARAERQE-----QSLLRHSVTNSQL-----GSPAPG---RHDRTLSKAGSDADGDSR 640

Db        588 PMEARAERAEVPDRPQSLLRHSITASQLQALDRGSPSPSPRPGHERSFSRVSEFGD-ISR 646

Qy        641 SDSPLPHFR-GKDSDWFYARREAASAILGLDQKISHLTDDELDALFDDVQKARAVRRGLV 699

Db        647 PETPSIFQRNGRESDWSLARREAAGAILGSDQNLTSLSDEELNALFEDVQKARAERVNVR 706

Qy        700 EDNEDSDSQSSFPVRDKYMSNGTIDNFSLDTAITMPGTPRSDDDGDAL------------ 747

Db        707 EDGDDSD--SSYPIREKYLSNGTMDNFSLDTALTMPSTPKQGEPDDRLREVREELQNKLE 764

Qy        748 ----FFGDKKSKQDASNVDVEELRQQQAQMEEALKTAKQE 783

Db        765 KQKEEYQDQLKSAEAANVEIEEIKQEKVKMEAALQELKED 804


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ID   Q86ZA3_COCHE   PRELIMINARY;   PRT;  1666 AA.
AC   Q86ZA3;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 17.
DE   Kinesin.
GN   Name=KLP8;
OS   Cochliobolus heterostrophus (Drechslera maydis).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC   Pleosporales; Pleosporaceae; Cochliobolus.
OX   NCBI_TaxID=5016;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22627967; PubMed=12742059; DOI=10.1016/S1087-1845(03)00022-7;
RA   Schoch C.L., Aist J.R., Yoder O.C., Gillian Turgeon B.;
RT   "A complete inventory of fungal kinesins in representative filamentous
RT   ascomycetes.";
RL   Fungal Genet. Biol. 39:1-15(2003).
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CC   ---------------------------------------------------------------------
DR   EMBL; AY230433; AAO59295.1; -; Genomic_DNA.
DR   HSSP; P33173; 1I5S.
DR   GO; GO:0005875; C:microtubule associated complex; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003777; F:microtubule motor activity; IEA.
DR   GO; GO:0007018; P:microtubule-based movement; IEA.
DR   InterPro; IPR000253; FHA.
DR   InterPro; IPR001752; kinesin_motor.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR011993; PH_type.
DR   Pfam; PF00498; FHA; 1.
DR   Pfam; PF00225; Kinesin; 1.
DR   Pfam; PF00169; PH; 1.
DR   PRINTS; PR00380; KINESINHEAVY.
DR   SMART; SM00129; KISc; 1.
DR   SMART; SM00233; PH; 1.
DR   PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR   PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
SQ   SEQUENCE   1666 AA;  186129 MW;  9F58CCCCF80F16EA CRC64;

  Query Match             67.5%;  Score 2721;  DB 2;  Length 1666;
  Best Local Similarity   69.8%;  Pred. No. 4.9e-130;
  Matches  552;  Conservative   77;  Mismatches  116;  Indels   46;  Gaps   11;

Qy         31 MEGNQTILTPPPGAEEKARKSGKTIMDGPKAFAFDRSYWSFDKNAPNYARQEDLFQDLGV 90

Db         65 MKGDQTILSPPANTDVKG-KAAKAAAEGVKTFAFDRSYWSFDRDAPNYAGQDNLHEDLGK 123

Qy         91 PLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYGKEHGVIPRICQDMFRRINELQKDKNLTC 150

Db        124 PLLDNAFQGYNNCIFAYGQTGSGKSYSMMGYGAEYGIIPKICQDMFERIKGMQQDKNSTC 183

Qy        151 TVEVSYLEIYNERVRDLLNPSTKGNLKVREHPSTGPYVEDLAKLVVRSFQEIENLMDEGN 210

Db        184 TVEVSYLEIYNERVRDLLNPSNKGNLRVREHPSTGPYVEDLAKLVVQSFSEIENLMDEGN 243

Qy        211 KARTVAATNMNETSSRSHAVFTLTLTQKWHDEETKMDTEKVAKISLVDLAGSERATSTGA 270

Db        244 KARTVAATNMNETSSRSHAVFTLTLTQKRHDVETSMSGERVAKISLVDLAGSERAQSTGA 303

Qy        271 TGARLKEGAEINRSLSTLGRVIAALADMSSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMT 330

Db        304 TGARLKEGAEINRSLSTLGRVIAALADQSSGKKKAQ--VPYRDSILTWLLKDSLGGNSMT 361

Qy        331 AMIAAISPADINFEETLSTLRYADSAKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQS 390

Db        362 AMIAAISPADINFEETLSTLRYADSAKRIKNHAVVNEDPNARMIRELKEELSKLRSQLGG 421

Qy        391 SGGGGGGAGGSGGPVEESYPPDTPLEKQIVSIQQPDATVKKMSKAEIVEQLNQSEKLYRD 450

Db        422 GGGGGGGAAGSNGIVEEQYPPDTPLEKQMVSITQADGSTKKVSKAEIAEQLTQSEKLYTE 481

Qy        451 LNQTWEEKLAKTEEIHKEREAALEELGISIEKGFVGPYHSKEMPHLVNLSDDPLLAECLV 510

Db        482 LNQTWEEKLQKTEEIHKEREAALEELGISIEKGFVGLSTPKNMPHLVNLSDDPLLTECLV 541

Qy        511 YNIKPGQTRVGNVNQDTQ-AEIRLNGSKILKEHCTFENVDNVVTIVPNEKAAVMVNGVRI 569

Db        542 YNLKPGTTTVGNSDVDGQTAQIRLNGSQILAEHCNFENVDGKVTVIPQEGASVMVNGVRI 601

Qy        570 DKPTRLRSGYRIILGDFHIFRFNHPEEARAERQE--QSLLRHSVTNSQLGS-----PAPG 622

Db        602 DKPRLLKSGHRIILGDFHIFRFNNPQEARAERAEVGTSLLRQTVTAGQLGSSPSPAPRPG 661

Qy        623 RHDR---TLSKAGSDADGDS-RSDSPLPHFRGKDSDWFYARREAASAILGLDQKISHLTD 678

Db        662 -HDRSYSSISVANSDFDPDSPRAGSPALWQRGRESEFSYARREALTAWLGPDKRIENLPD 720

Qy        679 DELDALFDDVQKARAVRRG-----LVEDNEDSDSQSSFPVRDKYMSNGTIDNFSLDTAIT 733

Db        721 EDFEALYEDLSRLRETRKARPESRMISDEGDTESMSSYPVREKYASGGTLDNFSLDTALT 780

Qy        734 MPGTPRSD-------------------DDGDALFFGDKKSKQDASNVDVEELRQQQAQM 773

Db        781 MPSTPHQDGSEKMQEIREEMQNKIDQSRDDFQARLKADEDAK-----VELQELRAAKEAM 835

Qy        774 EEALKTAKQEF 784

Db        836 QRQMKAQKEAF 846


RESULT 9
Q2UE08_ASPOR
ID   Q2UE08_ASPOR   PRELIMINARY;   PRT;  1519 AA.
AC   Q2UE08;
DT   24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT   24-JAN-2006, sequence version 1.
DT   07-MAR-2006, entry version 3.
DE   Kinesin-like protein.
GN   ORFNames=AO090026000806;
OS   Aspergillus oryzae.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX   NCBI_TaxID=5062;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=RIB 40;
RX   PubMed=16372010; DOI=10.1038/nature04300;
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RA   Machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terai G.,
RA   Kusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,
RA   Horiuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,
RA   Galagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,
RA   Bhatnagar D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,
RA   Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Juvvadi P.R.,
RA   Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,
RA   Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,
RA   Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,
RA   Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,
RA   Komori T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,
RA   Kuhara S., Ogasawara N., Kikuchi H.;
RT   "Genome sequencing and analysis of Aspergillus oryzae.";
RL   Nature 438:1157-1161(2005).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AP007159; BAE60207.1; -; Genomic_DNA.
SQ   SEQUENCE   1519 AA;  169635 MW;  F0A56250FF5859B6 CRC64;

  Query Match             65.4%;  Score 2634;  DB 2;  Length 1519;
  Best Local Similarity   67.7%;  Pred. No. 1.2e-125;
  Matches  536;  Conservative   58;  Mismatches   68;  Indels  130;  Gaps    9;

Qy          3 GGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKS--GKTIMDGPK 60
              |||||||||||||||:|| ||||:|||:|: |||:| ||||| :| ||:  ||  ::|||
Db          5 GGGNIKVVVRVRPFNSRENDRGAQCIVQMKENQTVLIPPPGAVDKLRKAGGGKGAVEGPK 64

Qy         61 AFAFDRSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
              |||||||||||||||||| |::|| ||||||||||:|||||||||||||||||||||||
Db         65 TFAFDRSYWSFDKNAPNYAGQDNLFDDLGVPLLDNAFQGYNNCIFAYGQTGSGKSYSMMG 124

Qy        121 YGKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
              ||||:|||||||| || || |:|:|||| |||||||||||||||||||| ||||||||
Db        125 YGKEYGVIPRICQSMFERITEIQQDKNLGCTVEVSYLEIYNERVRDLLNPSNKGNLKVRE 184

Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240
              |||||||||||||| |||||:|||||||||||||||||||||||||||||||||||||| |
Db        185 HPSTGPYVEDLAKLAVRSFEEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKRH 244

Qy        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS 300
              | || ||||||::|||||||||||||||||||||||||||||||||||||||||||::|
Db        245 DAETSMDTEKVSRISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADVAS 304

Qy        301 GKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKRIK 360
              ||:|   :|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 GKKKNASMVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKRIK 364

Qy        361 NHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGG---GGAGGS-----GGPVEESYPPD 412
              |||||||||||||||||||||:||    |||   | |||:     | | || ||||
Db        365 NHAVVNEDPNARMIRELKEELAQLRAKL----GGGVAPGAAGGAVAAAGGVPPEEYYPPD 420

Qy        413 TPLEKQIVSIQQPDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAA 472
              ||||||:||||:|| :: |:|||||||||||||:|||||||||| |||:||||||||
Db        421 TPLEKQVVSIQKPDGSITKVSKAEIVEQLNQSEKLYKDLNQTWEEKLVKTEQIHKEREAA 480

Qy        473 LEELGISIEKGFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIR 532
              ||||||||||||:|    |:|||||||||||||||||||| | |||::| :  |||
Db        481 LEELGISIEKGFIGLSTPKKMPHLVNLSDDPLLAECLVYNIKPGTTMVGNMDQGSHVEIR 540

Qy        533 LNGSKILKEHCTFENVDNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFN 592
              |||||||  || |||||||||||| | |||||||:||||| ||:||:|:|||||||||||
Db        541 LNGSKILANHCKFENVDNVVTIVPGEGAAVMVNGLRIDKPKRLKSGFRVILGDFHIFRFN 600

Qy        593 HPEEARAERQEQSLLRHSVTNSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHFRGKD 652
              ||:|||||| |                                 :| :  |: |   |
Db        601 HPQEARAERDED----------------------------EGQNGGDTALQSVR--- 626

Qy        653 SDWFYARREAASAILGLDQKISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDSQSSFP 712
                                                  |:|      | | :  |:   :
Db        627 ---------------------------------QDMQ------RQLDQQKEEYQEK---- 643
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Qy        713 VRDKYMSNGTIDNFSLDTAITMPGTPRSDDDGDALFFGDKKSKQDASNVDVEELRQQQAQ 772
              :|:  :|:|                                          || :| ::|:
Db        644 LRNAELSSGQ----------------------------------------GVENIRSEKAR 664

Qy        773 MEEALKTAKQEF 784
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Db        665 MEEALRAAKEEF 676


RESULT 10
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ID   Q4P0W2_USTMA   PRELIMINARY;   PRT;  1676 AA.
AC   Q4P0W2;
DT   19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Hypothetical protein.
GN   ORFNames=UM06251.1;
OS   Ustilago maydis 521.
OC   Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC   Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX   NCBI_TaxID=237631;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=521;
RA   Birren B.W., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA   Ait-Zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
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RA   Venkataraman V.S., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA   Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA   Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA   Zimmer A., Zody M., Lander E.S.;
RT   "The genome sequence of Ustilago maydis.";
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AACP01000237; EAK87131.1; -; Genomic_DNA.
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DR   GO; GO:0005875; C:microtubule associated complex; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003777; F:microtubule motor activity; IEA.
DR   GO; GO:0007018; P:microtubule-based movement; IEA.
DR   InterPro; IPR000253; FHA.
DR   InterPro; IPR001752; kinesin_motor.
DR   InterPro; IPR001849; PH.
DR   Pfam; PF00498; FHA; 1.
DR   Pfam; PF00225; Kinesin; 1.
DR   Pfam; PF00169; PH; 1.
DR   PRINTS; PR00380; KINESINHEAVY.
DR   SMART; SM00129; KISc; 1.
DR   SMART; SM00233; PH; 1.
DR   PROSITE; PS50006; FHA_DOMAIN; 1.
DR   PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR   PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   1676 AA;  184606 MW;  A44A5CD7B2EA99AE CRC64;

  Query Match             48.6%;  Score 1957.5;  DB 2;  Length 1676;
  Best Local Similarity   51.8%;  Pred. No. 4.9e-91;
  Matches  426;  Conservative  111;  Mismatches  194;  Indels   91;  Gaps   19;

Qy          1 MSGGGNIKVVVRVRPFNAREIDRGAKCIVR-MEGNQTILTPPPGAEEKARKSGKTIMDGP 59
              |:  |||||||| || |:|| :|||  ::  :: :| ||:||  |: |  :: |
Db          1 MADSGNIKVVVRCRPMNSRERNRGASNLIEFVDQHQLILSPPNEADTK--ENSKATKKKS 58

Qy         60 KAFAFDRSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMM 119
                |:|||:|         :  |:|||| :|| || :|| |:| |:||||||||||:||:
Db         59 MPFSFDRAY-------DEHTEQDDLFQYIGVELLQHAFNGFNTCVFAYGQTGSGKSHSMV 111

Qy        120 GYGKEHGVIPRICQDMFRRINE-LQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
              || :  |:||  |  :|  ||:   | ||  :|||||:|||||:|||||||  ||||||
Db        112 GYAQAKGIIPLTCARLFEDINQKTAADPNLKISVEVSYIEIYNEKVRDLLNPKNKGNLKV 171

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
              ||||| |||||||:|||| |: :| ||||||||||||||||||||||||||||||| ||||
Db        172 REHPSLGPYVEDLSKLVVASYPDIMNLMDEGNKARTVAATNMNETSSRSHAVFTLVLTQK 231

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
                | :||:: |||::||:|||||||| |||||||||||| |||||:|||:||||||
Db        232 RFDVQTKLEAEKVSRISMVDLAGSERANSTGATGARLKEGANINRSLTTLGKVIAALAIA 291

Qy        299 SS-------GKQKK----NQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETL 347
              ||          |: |    :  |||||||||||||||||||| ||||||||||  :||||
Db        292 SSAVEPVKGAKKPKTASLDSFVPYRDSVLTWLLKDSLGGNSKTAMIAAISPAD--YEETL 349

Qy        348 STLRYADSAKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGAGGSGGPVEE 407
              ||||||| ||:||| |||||||||::||||||||  ||:::     |||||  |      |
Db        350 STLRYADQAKKIKNKAVVNEDPNAKLIRELKEELELLRTRV----SGGGGADG-----ES 400

Qy        408 SYPPDTPLEKQIVSIQQPDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHK 467
              :: |  | :||:|  |      :| ::|||: ||| ||||:   ||::||||| ||:|| |
Db        401 NWDPSIPPDKQVVRYQTKTGEIKTVTKAELQEQLEQSEKIMSSLNESWEEKLTKTQEIQK 460

Qy        468 EREAALEELGISIEKGFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDT 527
              ||| ||||||||::|| || :  |::||||||::|||::||:| |||| | |||::
Db        461 EREKALEELGISVDKGNVGVHTPKKLPHLVNLNEDPLMSECLIYQIKPGHTLVGNLDSGP 520

Qy        528 QAEIRLNGSKILKEHCTFENVDNVVTIVPNEKAAVMVNGVRI--DKPTRLRSGYRIILGD 585
                |:|:|:||| :|| |:: | :||:     :  |||| |:  |:| ||||||:|||
Db        521 DVHIKLSGTKILNKHCMFDHQDGLVTVTAMPDSMTMVNGKRLAPDEPKRLRSGYRVILGD 580

Qy        586 FHIFRFNHPEEARAERQEQSLLRHSVTNSQLGSPAPGRHDRTLSKAGSDADGD---SRSD 642
              ||:|||||||| |  |                | |       |: ||       |||   :| |
Db        581 FHVFRFNHPEEVRKARDR--------VRSTLALSTGEAHNETL------IDGDLPSTRPD 626

Qy        643 SPLPHFRGKDSDWFYARREAASAIL-GLDQKISHLTDDELDALFDDVQKARA-------- 693
              ||       | || |||||   | | | :    :| :::|: ||:|: :||:
Db        627 SP----ASGDVDWTYARREYTMAKLNGQNVNFDNLNEEDLEKLFEDISRARSKKSMGSVL 682

Qy        694 ----VRRGLVEDNEDSDSQSSFPVRDKYMSNGTIDNFSLDTAITMPGTPRSDDDGDALFF 749
                        | | :||    |:|:  |   |       |: |:|     | :    : |   |
Db        683 GRPESRASLFDDNA---SESASSVIRPYSHGALTDDTSID-----PWSQAGSEMGSMRFS 734

Qy        750 GDKKSKQD-------------ASNVDVEELRQQQAQMEEAL 777
                    |::               ||: : | || :  : || |
Db        735 AGTPIKENAYTGAGASSPALVAASHRETESLRAKVREYEEKL 776


RESULT 11
Q8TG36_USTMA
ID   Q8TG36_USTMA   PRELIMINARY;   PRT;  1676 AA.
AC   Q8TG36;
DT   01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2002, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   Kinesin.
GN   Name=kin3;
OS   Ustilago maydis (Smut fungus).
OC   Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC   Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX   NCBI_TaxID=5270;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22060494; PubMed=12065408; DOI=10.1093/emboj/cdf296;
RA   Wedlich-Soldner R., Straube A., Friedrich M.W., Steinberg G.;
RT   "A balance of KIF1A-like kinesin and dynein organizes early endosomes
RT   in the fungus Ustilago maydis.";
RL   EMBO J. 21:2946-2957(2002).
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF480446; AAL87137.1; -; Genomic_DNA.
DR   HSSP; P33173; 1I6I.
DR   GO; GO:0005875; C:microtubule associated complex; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003777; F:microtubule motor activity; IEA.
DR   GO; GO:0007018; P:microtubule-based movement; IEA.
DR   InterPro; IPR000253; FHA.
DR   InterPro; IPR001752; kinesin_motor.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR011993; PH_type.
DR   Pfam; PF00498; FHA; 1.
DR   Pfam; PF00225; Kinesin; 1.
DR   Pfam; PF00169; PH; 1.
DR   PRINTS; PR00380; KINESINHEAVY.
DR   SMART; SM00129; KISc; 1.
DR   SMART; SM00233; PH; 1.
DR   PROSITE; PS50006; FHA_DOMAIN; 1.
DR   PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR   PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
SQ   SEQUENCE   1676 AA;  184606 MW;  A44A5CD7B2EA99AE CRC64;

  Query Match             48.6%;  Score 1957.5;  DB 2;  Length 1676;
  Best Local Similarity   51.8%;  Pred. No. 4.9e-91;
  Matches  426;  Conservative  111;  Mismatches  194;  Indels   91;  Gaps   19;

Qy          1 MSGGGNIKVVVRVRPFNAREIDRGAKCIVR-MEGNQTILTPPPGAEEKARKSGKTIMDGP 59
              |:  |||||||| || |:|| :|||  ::  :: :| ||:||  |: |  :: |
Db          1 MADSGNIKVVVRCRPMNSRERNRGASNLIEFVDQHQLILSPPNEADTK--ENSKATKKKS 58

Qy         60 KAFAFDRSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMM 119
                |:|||:|         :  |:|||| :|| || :|| |:| |:||||||||||:||:
Db         59 MPFSFDRAY-------DEHTEQDDLFQYIGVELLQHAFNGFNTCVFAYGQTGSGKSHSMV 111

Qy        120 GYGKEHGVIPRICQDMFRRINE-LQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
              || :  |:||  |  :|  ||:   | ||  :|||||:|||||:|||||||  ||||||
Db        112 GYAQAKGIIPLTCARLFEDINQKTAADPNLKISVEVSYIEIYNEKVRDLLNPKNKGNLKV 171

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
              ||||| |||||||:|||| |: :| ||||||||||||||||||||||||||||||| ||||
Db        172 REHPSLGPYVEDLSKLVVASYPDIMNLMDEGNKARTVAATNMNETSSRSHAVFTLVLTQK 231
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Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
Db        232 RFDVQTKLEAEKVSRISMVDLAGSERANSTGATGARLKEGANINRSLTTLGKVIAALAIA 291

Qy        299 SS-------GKQKK----NQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETL 347
Db        292 SSAVEPVKGAKKPKTASLDSFVPYRDSVLTWLLKDSLGGNSKTAMIAAISPAD--YEETL 349

Qy        348 STLRYADSAKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGAGGSGGPVEE 407
Db        350 STLRYADQAKKIKNKAVVNEDPNAKLIRELKEELELLRTRV----SGGGGADG-----ES 400

Qy        408 SYPPDTPLEKQIVSIQQPDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHK 467
Db        401 NWDPSIPPDKQVVRYQTKTGEIKTVTKAELQEQLEQSEKIMSSLNESWEEKLTKTQEIQK 460

Qy        468 EREAALEELGISIEKGFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDT 527
Db        461 EREKALEELGISVDKGNVGVHTPKKLPHLVNLNEDPLMSECLIYQIKPGHTLVGNLDSGP 520

Qy        528 QAEIRLNGSKILKEHCTFENVDNVVTIVPNEKAAVMVNGVRI--DKPTRLRSGYRIILGD 585
Db        521 DVHIKLSGTKILNKHCMFDHQDGLVTVTAMPDSMTMVNGKRLAPDEPKRLRSGYRVILGD 580

Qy        586 FHIFRFNHPEEARAERQEQSLLRHSVTNSQLGSPAPGRHDRTLSKAGSDADGD---SRSD 642
Db        581 FHVFRFNHPEEVRKARDR--------VRSTLALSTGEAHNETL------IDGDLPSTRPD 626

Qy        643 SPLPHFRGKDSDWFYARREAASAIL-GLDQKISHLTDDELDALFDDVQKARA-------- 693
Db        627 SP----ASGDVDWTYARREYTMAKLNGQNVNFDNLNEEDLEKLFEDISRARSKKSMGSVL 682

Qy        694 ----VRRGLVEDNEDSDSQSSFPVRDKYMSNGTIDNFSLDTAITMPGTPRSDDDGDALFF 749
Db        683 GRPESRASLFDDNA---SESASSVIRPYSHGALTDDTSID-----PWSQAGSEMGSMRFS 734

Qy        750 GDKKSKQD--------------ASNVDVEELRQQQAQMEEAL 777
Db        735 AGTPIKENAYTGAGASSPALVAASHRETESLRAKVREYEEKL 776
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RESULT 12
Q55Z46_CRYNE
ID   Q55Z46_CRYNE   PRELIMINARY;   PRT;  1556 AA.
AC   Q55Z46;
DT   24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   24-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Hypothetical protein.
GN   ORFNames=CNBA6420;
OS   Cryptococcus neoformans var. neoformans B-3501A.
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC   Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX   NCBI_TaxID=283643;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=B-3501A;
RA   Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
RA   Wickes B.L., Fu J., Davis R.W.;
RT   "Cryptococcus neoformans serotype D sequencing.";
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AAEY01000004; EAL23117.1; -; Genomic_DNA.
DR   GO; GO:0005875; C:microtubule associated complex; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003777; F:microtubule motor activity; IEA.
DR   GO; GO:0007018; P:microtubule-based movement; IEA.
DR   InterPro; IPR001752; kinesin_motor.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR011993; PH_type.
DR   Pfam; PF00498; FHA; 1.
DR   Pfam; PF00225; Kinesin; 1.
DR   Pfam; PF00169; PH; 1.
DR   PRINTS; PR00380; KINESINHEAVY.
DR   SMART; SM00129; KISc; 1.
DR   SMART; SM00233; PH; 1.
DR   PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR   PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   1556 AA;  174143 MW;  A91B63EB61330354 CRC64;
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  Query Match             48.0%;  Score 1932.5;  DB 2;  Length 1556;
  Best Local Similarity   53.0%;  Pred. No. 8.4e-90;
  Matches  420;  Conservative   99;  Mismatches  190;  Indels   83;  Gaps   14;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
Db          3 GGNIKVVVRCRPLNAREIARGSKELIRMEGSQTILDPP---EATGGASSKAIEKKPMIFS 59

Qy         64 FDRSYWSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122
Db         60 FDKSYWSAGPKDDPKYASQQTLYEDLGADLLDHSFEGFNTCIFAYGQTGSGKSYSMMGYG 119

Qy        123 KEHGVIPRICQDMFRRIN-ELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVREH 181
Db        120 AEKGIIPLTTSELFRRIEARMGSDVNLSYTVEVSYIEIYNEKVRDLLNPKNKGNLRVREH 179

Qy        182 PSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTL--TLTQKW 239
Db        180 PSLGPYVEDLSRLVVENYTQMMTLMDEGNKARTVASTNMNETSSRSHAVFTLVVSLTQKR 239

Qy        240 HDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMS 299
Db        240 HDPQTQMTGEKVSKISLVDLAGSERQASTGATGTRLKEGANINKSLTTLGKVISALAQAG 299

Qy        300 SGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKRI 359
Db        300 QNKRKKEEHVPYRDSVLTWLLKESLGGNSKTAMIAAISPAD--YEETLSTLRYADAAKKI 357

Qy        360 KNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGAGGSGGPVEESYPPDTPLEKQI 419
Db        358 KTHAIVNEDPNAKLIRELKEELELLRSRVLMSGLSD----------ESSYDPSIPPEKQI 407

Qy        420 VSIQQPDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGIS 479
Db        408 VTYITKEGEIRKVTKLELQDQLEASEKLMESLNLTWEEKLQKTQAIHIEREKALEELGIS 467

Qy        480 IEKGFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKIL 539
Db        468 IDTNMVGVHAPQNHPSLVNLNEDPLMSECLIYQIKPGTTIAGAVDED-KAHIKLSGTHIL 526

Qy        540 KEHCTFENVDNVVTIVPNEKAAVMVNGVRI--DKPTRLRSGYRIILGDFHIFRFNHPEEA 597
Db        527 PEHCSFTNDEGVVTIEAMPDARTFVNGKRVPPNSPVKLLNGFRVILGDSHVFRFNDPAAV 586

Qy        598 RAERQEQSLLRHSVTNSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHFRGKDSDWFY 657
Db        587 RAERKK---LRISSSTDENGSLTPG---------------LRPDSPSSRVDTELMDWTA 627

Qy        658 ARREAASAILGLDQKISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDSQSSFPVRDKY 717
Db        628 ARREVAD--------IEKLADQDLDKLYDDILKLRTQRRRPESRMDIADFDSHFERSANP 679

Qy        718 MSN--------GTIDNFSLDTAITMPGTPRSDDDGDALFFGDKKSKQDASNVDVEEL-RQ 768
Db        680 LSNPWAGPGQTATMTSNSLATPV-----------------------GPDVDVNIVDEQ 714

Qy        769 QQAQMEEALKTA 780
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                :   |:|| |:
Db        715 SETSAEQALHTS 726


RESULT 13
Q5KNG1_CRYNE
ID   Q5KNG1_CRYNE   PRELIMINARY;   PRT;  1556 AA.
AC   Q5KNG1;
DT   15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT   15-FEB-2005, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   Kinesin, putative.
GN   OrderedLocusNames=CNA06610;
OS   Cryptococcus neoformans (Filobasidiella neoformans).
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC   Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX   NCBI_TaxID=5207;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=JEC21;
RX   PubMed=15653466; DOI=10.1126/science.1103773;
RA   Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
RA   Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
RA   Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
RA   D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
RA   Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
RA   Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,
RA   Mathewson C.A., Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L.,
RA   Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
RA   Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
RA   Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
RA   Fraser C.M., Hyman R.W.;
RT   "The genome of the basidiomycetous yeast and human pathogen
RT   Cryptococcus neoformans.";
RL   Science 307:1321-1324(2005).
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CC   ---------------------------------------------------------------------
DR   EMBL; AE017341; AAW41182.1; -; Genomic_DNA.
DR   GO; GO:0005875; C:microtubule associated complex; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003777; F:microtubule motor activity; IEA.
DR   GO; GO:0007018; P:microtubule-based movement; IEA.
DR   InterPro; IPR000253; FHA.
DR   InterPro; IPR001752; kinesin_motor.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR011993; PH_type.
DR   Pfam; PF00498; FHA; 1.
DR   Pfam; PF00225; Kinesin; 1.
DR   Pfam; PF00169; PH; 1.
DR   PRINTS; PR00380; KINESINHEAVY.
DR   SMART; SM00129; KISc; 1.
DR   SMART; SM00233; PH; 1.
DR   PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR   PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
KW   Complete proteome.
SQ   SEQUENCE   1556 AA;  174210 MW;  D4E65A002B91115B CRC64;

  Query Match             47.0%;  Score 1895;  DB 2;  Length 1556;
  Best Local Similarity   52.2%;  Pred. No. 6.9e-88;
  Matches  412;  Conservative   97;  Mismatches  191;  Indels   90;  Gaps   13;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              ||||||||| || ||||| ||:| ::||||:|||| ||    |      | | |    |  |:
Db          3 GGNIKVVVRCRPLNAREIARGSKELIRMEGSQTILDPP---EATGGASSKAIEKKPMIFS 59

Qy         64 FDRSYWSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122
              ||:||||    |: | || |: |::|||  |||::|:|:| ||||||||||||||||||
Db         60 FDKSYWSAGPKDDPRYASQQTLYEDLGADLLDHSFEGFNTCIFAYGQTGSGKSYSMMGYG 119

Qy        123 KEHGVIPRICQDMFRRIN-ELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVREH 181
                | |:||    ::|||    :  | ||: ||||||:|||||:|||||||  ||||:||||
Db        120 AEKGIIPLTTSELFRRIEARMGSDVNLSYTVEVSYIEIYNEKVRDLLNPKNKGNLRVREH 179

Qy        182 PSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWHD 241
              || |||||||::||| :: ::  |||||||||||:|||||||||||||||| |||| ||
Db        180 PSLGPYVEDLSRLVVENYTQMMTLMDEGNKARTVASTNMNETSSRSHAVFTLVLTQKRHD 239

Qy        242 EETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSSG 301
              :|:|  |||:||||||||||||  |||||| |||||| ||:||:|||:||:|||
Db        240 PQTQMTGEKVSKISLVDLAGSERQASTGATGTRLKEGANINKSLTTLGKVISALAQAGQN 299

Qy        302 KQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKRIKN 361
              |:|| : ||||||||||||:|||||| |||||||           |||||||:||:||
Db        300 KRKKEEHVPYRDSVLTWLLKESLGGNSKTAMIAAI-----------STLRYADAAKKIKT 348

Qy        362 HAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGAGGSGGPVEESYPPDTPLEKQIVS 421
              ||:||||||::|||||||  |||::  ||              | || |  | |||||:
Db        349 HAIVNEDPNAKLIRELKEELELLRSRVLMSGLSD----------ESSYDPSIPPEKQIVT 398

Qy        422 IQQPDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISIE 481
                :  ::|::| |: :||  ||||   || |||||| ||: || ||| |||||||||:
Db        399 YITKEGEIRKVTKLELQDQLEASEKLMESLNLTWEEKLQKTQAIHIEREKALEELGISID 458

Qy        482 KGFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKILKE 541
              || :  :  | ||||::|||::|||:| |||| |  | |::| :| |:|:|: || |
Db        459 TNMVGVHAPQNHPSLVNLNEDPLMSECLIYQIKPGTTIAGAVDED-KAHIKLSGTHILPE 517

Qy        542 HCTFENVDNVVTIVPNEKAAVMVNGVRI--DKPTRLRSGYRIILGDFHIFRFNHPEEARA 599
              ||:| | : ||||      |    ||| |:  : | :| :|:|:|||| |:|||| |   ||
Db        518 HCSFTNDEGVVTIEAMPDARTFVNGKRVPPNSPVKLLNGFRVILGDSHVFRFNDPAAVRA 577

Qy        600 ERQEQSLLRHSVTNSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHFRGKDSDWFYAR 659
              ||::   || | :  : ||  ||                | |||      :  ||  ||
Db        578 ERKK---LRISSSTDENGSLTPG---------------LRPDSPSSRVDTELMDWTAAR 618

Qy        660 REAASAILGLDQKISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDSQSSFPVRDKYMS 719
              || |          |  | | :|| |:||: | |  |       : :|  | |      :|
Db        619 REVAD--------IEKLADQDLDKLYDDILKLRTQRRRPESRMDIADFDSHFERSANPLS 670

Qy        720 N--------GTIDNFSLDTAITMPGTPRSDDDGDALFFGDKKSKQDASNVDVEEL-RQQQ 770
              |         |: : || | :                              :|||  :  | :
Db        671 NPWAGPGQTATMTSNSLATPV-----------------------GPDVDVNIVDEQSE 705

Qy        771 AQMEEALKTA 780
                |:|| |:
Db        706 TSAEQALHTS 715


RESULT 14
Q4VXC3_HUMAN
ID   Q4VXC3_HUMAN   PRELIMINARY;   PRT;  1153 AA.
AC   Q4VXC3;
DT   05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Kinesin family member 1B.
GN   Name=KIF1B; ORFNames=RP4-736L20.1-003;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Dunn M.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AL358013; CAI95222.1; -; Genomic_DNA.
DR   SMR; Q4VXC3; 4-347.
DR   GO; GO:0005874; C:microtubule; IEA.
```

```
DR   GO; GO:0005875; C:microtubule associated complex; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003777; F:microtubule motor activity; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0007018; P:microtubule-based movement; IEA.
DR   InterPro; IPR000253; FHA.
DR   InterPro; IPR001752; kinesin_motor.
DR   Pfam; PF00498; FHA; 1.
DR   Pfam; PF00225; Kinesin; 1.
DR   PRINTS; PR00380; KINESINHEAVY.
DR   SMART; SM00240; FHA; 1.
DR   SMART; SM00129; KISc; 1.
DR   PROSITE; PS50006; FHA_DOMAIN; 1.
DR   PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR   PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW   ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ   SEQUENCE   1153 AA;  130363 MW;  6F0D8846CD283811 CRC64;

  Query Match           42.0%;  Score 1691;  DB 2;  Length 1153;
  Best Local Similarity   43.6%;  Pred. No. 1.2e-77;
  Matches  382;  Conservative  137;  Mismatches  235;  Indels  122;  Gaps   19;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||  : :|||::|:|| | :  |   :|            ||:|:
Db          3 GASVKVAVRVRPFNSRETSKESKCIIQMQGNSTSIINPKNPKE----------APKSFS 51

Qy         64 FDRSYWSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122
              || ||||      | :| |  :: |:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWSHTSPEDPCFASQNRVYNDIGKEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGKQ 111

Qy        123 KEH--GVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
              :|   |:||::|:::| :||:   :: :: :|||||:||| |||||||||  ||||:|||
Db        112 EESQAGIIPQLCEELFEKIND-NCNEEMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE 170

Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240
              ||  |||||||:|| | |: :| :||| ||||||||||||||||||||||:  ||| |
Db        171 HPLLGPYVEDLSKLAVTSYTDIADLMDAGNKARTVAATNMNETSSRSHAVFTIVFTQKKH 230

Qy        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS 300
              | || : ||||:|||||||||||||| |||| | |||||| ||:||:|||:||:|||::|
Db        231 DNETNLSTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEVSK 290

Qy        301 GKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKRIK 360
              |:||   :|||||||||||:::||||| |||:||:||||||::|||||||||| ||:||
Db        291 -KKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADRAKQIK 349

Qy        361 NHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGAGGSGGPVEESYPPDTPLEKQ-- 418
              :||:||||||:::|||||: :|:  |:: | |       |     | |    |  |
Db        350 CNAVINEDPNAKLVRELKEEVTRLKDLLRAQGLGDIIDTSMGSLT--SSPSSCSLSSQVG 407

Qy        419 ---IVSIQQPDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEE 475
                 : |||  :  :      | :|:| :|||:  :||:|||||| ||| |  |||| | |
Db        408 LTSVTSIQ--ERIMSTPGGEEAIERLKESEKIIAELNETWEEKLRKTEAIRMEREALLAE 465

Qy        476 LGISIEK--GFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRL 533
              :|::|  :  | :|  :  |: |||||::|||::|||:| || | ||||  : : : :| |
Db        466 MGVAIREDGGTLGVFSPKKTPHLVNLNEDPLMSECLLYYIKDGITRVGQADAERRQDIVL 525

Qy        534 NGSKILKEHCTFENV-----DNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHI 588
              :|: | :||| | :      : :||: | |::   ||| |: :| :|||| |||:|  |:
Db        526 SGAHIKEEHCIFRSERSNSGEVIVTLEPCERSETYVNGKRVSQPVQLRSGNRIIMGKNHV 585

Qy        589 FRFNHPEEARAER----------------QEQSLLRHSVTNSQ----------LGSP 619
              |||||||:|||||                | : | :  :   |           |
Db        586 FRFNHPEQARAEREKTPSAETPSEPVDWTFAQRELLEKQGIDMKQEMEKRLQEMEILYKK 645

Qy        620 APGRHDRTLSKAGSDADGDSRSDS---------------------------------- 643
                  |  | :   ||| ||  ||
Db        646 EKEEADLLLEQQRLDADSDSGDDSDKRSCEESWKLITSLREKLPPSKLQTIVKKCGLPSS 705

Qy        644 ----------PLPHFR--GKDSDWFYARREAASAILGLDQKISHLTD-----DELDALFD 686
                       :|  |   ||| |      |:  :  ::: | |      |::||
Db        706 GKKREPIKMYQIPQRRRLSKDSKWVTISDLKIQAVKEICYEVA-LNDFRHSRQEIEALAI 764
```

```
Qy        687 DVQKARAVRRGLVEDNEDSDSQSSFPVRDKYMSNGTIDNFSLDTAITMPGTPRSDD---- 742
                  |       |  : ||  ||  :   || : : |  |     |   |  |:   ||
Db        765 VKMKELCAMYGKKDPNE-RDSWRAV-ARDVWDTVGVGDEKIEDVMATGKGSTDVDDLKVH 822

Qy        743 -DGDALFFGDKKSKQDASNVDVEELRQQQAQMEEAL 777
               |       : | : :  : ::: || :  :||: |
Db        823 IDKLEDILQEVKKQNNMKDEEIKVLRNKMLKMEKVL 858


RESULT 15
Q4R9M8_HUMAN
ID   Q4R9M8_HUMAN   PRELIMINARY;   PRT;  1797 AA.
AC   Q4R9M8;
DT   19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 6.
DE   Kinesin family member 1Bbeta isoform III.
GN   Name=KIF1Bbeta;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Munirajan A.K., Ohira M., Nakagawara A.;
RT   "Identification of splicing variants of KIF1Bbeta.";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB088212; BAE02545.1; -; mRNA.
DR   SMR; Q4R9M8; 4-353.
DR   GO; GO:0005875; C:microtubule associated complex; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003777; F:microtubule motor activity; IEA.
DR   GO; GO:0007018; P:microtubule-based movement; IEA.
DR   InterPro; IPR000253; FHA.
DR   InterPro; IPR001752; kinesin_motor.
DR   InterPro; IPR001849; PH.
DR   Pfam; PF00498; FHA; 1.
DR   Pfam; PF00225; Kinesin; 1.
DR   Pfam; PF00169; PH; 1.
DR   PRINTS; PR00380; KINESINHEAVY.
DR   SMART; SM00240; FHA; 1.
DR   SMART; SM00129; KISc; 1.
DR   SMART; SM00233; PH; 1.
DR   PROSITE; PS50006; FHA_DOMAIN; 1.
DR   PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR   PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
SQ   SEQUENCE   1797 AA;  201951 MW;  370ACF5BB0ED6D15 CRC64;

  Query Match           41.8%;  Score 1683.5;  DB 2;  Length 1797;
  Best Local Similarity   46.4%;  Pred. No. 5.3e-77;
  Matches  355;  Conservative  126;  Mismatches  173;  Indels  111;  Gaps   15;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||  : :|||::|:|| | :  |   :|            ||:|:
Db          3 GASVKVAVRVRPFNSRETSKESKCIIQMQGNSTSIINPKNPKE----------APKSFS 51

Qy         64 FDRSYWSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122
              || ||||      | :| |  :: |:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWSHTSPEDPCFASQNRVYNDIGKEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGKQ 111

Qy        123 KEH--GVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
              :|   |:||::|:::| :||:   :: :: :|||||:||| |||||||||  ||||:|||
Db        112 EESQAGIIPQLCEELFEKIND-NCNEEMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE 170

Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240
              ||  |||||||:|| | |: :| :||| ||||||||||||||||||||||:  ||| |
```

```
Db        171 HPLLGPYVEDLSKLAVTSYTDIADLMDAGNKARTVAATNMNETSSRSHAVFTIVFTQKKH 230

Qy        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM-- 298

Db        231 DNETNLSTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEVDN 290

Qy        299 ---SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADS 355

Db        291 CTSKSKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADR 350

Qy        356 AKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGG------------GGGAGGSG 402

Db        351 AKQIKCNAVINEGPNAKLVRELKEEVTRLKDLLRAQGLGDIIDIDPLIDDYSGSGSKSSM 410

Qy        403 GPVEESYPPDTPLEKQ-----IVSIQQPDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEE 457

Db        411 GSLTSS-PSSCSLSSQVGLTSVTSIQ--ERIMSTPGGEEAIERLKESEKIIAELNETWEE 467

Qy        458 KLAKTEEIHKEREAALEELGISIEK--GFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKP 515

Db        468 KLRKTEAIRMEREALLAEMGVAIREDGGTLGVFSPKKTPHLVNLNEDPLMSECLLYYIKD 527

Qy        516 GQTRVGNVNQDTQAEIRLNGSKILKEHCTFENV-----DNVVTIVPNEKAAVMVNGVRID 570

Db        528 GITRVGQADAERRQDIVLSGAHIKEEHCIFRSERSNSGEVIVTLEPCERSETYVNGKRVS 587

Qy        571 KPTRLRSGYRIILGDFHIFRFNHPEEARAERQEQSLLRHSVTNSQLGSPAPGRHDRTLSK 630

Db        588 QPVQLRSGNRIIMGKNHVFRFNHPEQARAEREK-------------------------- 620

Qy        631 AGSDADGDSRSDSPLPHFRGKDSDWFYARREAASAILGLDQK------------ISHLTD 678

Db        621 ------------TPSAETPSEPVDWTFAQRELLEK-QGIDMKQEMEKRLQEMEILYKKEK 667

Qy        679 DELDALFDD-----------VQKARAVRRGLVEDNEDSDSQSSFP 712

Db        668 EEADLLLEQQRLDYESKLQALQKQVETRSLAAETTEEEEEEEEVP 712
```

Search completed: September 1, 2006, 14:33:39
Job time : 269.166 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: September 5, 2006, 18:01:01 ; Search time 196 Seconds
(without alignments)
832.787 Million cell updates/sec

Title: US-09-235-416-1_COPY_1_357
Perfect score: 1834
Sequence: 1 MSGGGNIKVVVRVRPFNARE.....PADINFEETLSTLRYADSAK 357

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1834	100.0	784	2	AAY06618	Aay06618 Thermomyc
2	1152	62.8	421	4	AAM41820	Aam41820 Human pol
3	1152	62.8	1699	8	ABM83651	Abm83651 Human dia
4	1152	62.8	1708	8	ABM83650	Abm83650 Human dia
5	1152	62.8	1714	8	ABM83648	Abm83648 Human dia
6	1152	62.8	1721	8	ABM83647	Abm83647 Human dia
7	1149	62.6	893	4	AAM40034	Aam40034 Human pol
8	1142	62.3	1696	8	ABM83653	Abm83653 Human dia
9	1142	62.3	1697	8	ABM83652	Abm83652 Human dia
10	1142	62.3	1709	8	ABM83649	Abm83649 Human dia
11	1142	62.3	1722	8	ABM83646	Abm83646 Human dia
12	1119	61.0	1199	8	ABM83671	Abm83671 Human dia
13	1119	61.0	1816	3	AAB36227	Aab36227 Human kin
14	1119	61.0	1823	5	ABB07867	Abb07867 Human kin
15	1117	60.9	1103	3	AAY51328	Aay51328 Human KLI
16	1117	60.9	1103	4	AAE04316	Aae04316 Human kin
17	1117	60.9	1103	6	ABG72054	Abg72054 Human kin
18	1117	60.9	1103	7	ADG63388	Adg63388 Human kin
19	1114	60.7	1770	6	AAE35317	Aae35317 Mouse KIF
20	1112.5	60.7	1805	7	ADJ95088	Adj95088 Novel NOV
21	1111	60.6	365	9	ADV50414	Adv50414 Human KIF
22	1106.5	60.3	1773	4	ABB63908	Abb63908 Drosophil
23	1063	58.0	1362	5	AAU74840	Aau74840 Human HsK
24	1063	58.0	1805	5	ABP68930	Abp68930 Human pol
25	1028	56.1	1921	4	ABB62962	Abb62962 Drosophil
26	1027.5	56.0	757	4	AAU19569	Aau19569 Human dia
27	1027.5	56.0	757	5	ABP51294	Abp51294 Human MDD
28	1020.5	55.6	762	5	ABG60124	Abg60124 Human DIT
29	1016.5	55.4	1826	7	ADJ69671	Adj69671 Human hea
30	1016.5	55.4	1826	8	ADL83235	Adl83235 Human PRO
31	1012	55.2	1844	8	ADQ97522	Adq97522 Mouse can
32	1010.5	55.1	1507	8	ADQ97525	Adq97525 Human can
33	990.5	54.0	1815	8	ADR66952	Adr66952 Human pro
34	990.5	54.0	1815	8	ADR66054	Adr66054 Human pro
35	990.5	54.0	1815	8	ADR66951	Adr66951 Human pro
36	990.5	54.0	1815	8	ADR66053	Adr66053 Human pro
37	987	53.8	359	5	ABB79530	Abb79530 Human kin
38	987	53.8	359	5	ABB84482	Abb84482 Human HsK
39	987	53.8	359	5	AAE22526	Aae22526 Human HsK
40	987	53.8	944	7	ADM04401	Adm04401 Human pro
41	987	53.8	944	9	AEC87331	Aec87331 Human cDN
42	987	53.8	1317	9	AED07567	Aed07567 Chromosom
43	987	53.8	1392	6	AAE32129	Aae32129 Human cyt
44	987	53.8	1392	7	ADJ94858	Adj94858 Novel NOV
45	987	53.8	1393	8	ADN00367	Adn00367 Novel hum
46	951.5	51.9	1375	5	ABB79531	Abb79531 Human kin
47	951.5	51.9	1375	5	ABB84481	Abb84481 Human HsK
48	951.5	51.9	1375	5	AAE22525	Aae22525 Human HsK
49	947	51.6	1394	7	ADJ94856	Adj94856 Novel NOV
50	913.5	49.8	503	3	AAB63190	Aab63190 Human sec
51	911.5	49.7	504	3	AAB63189	Aab63189 Gene 5 hu
52	873	47.6	1174	4	ABB61704	Abb61704 Drosophil
53	835	45.5	366	9	ADV50400	Adv50400 Human KIF
54	835	45.5	376	9	ADV50399	Adv50399 Human KIF
55	834	45.5	354	9	ADV50396	Adv50396 Human KIF
56	834	45.5	378	9	ADV50398	Adv50398 Human KIF
57	834	45.5	388	9	ADV50397	Adv50397 Human KIF
58	834	45.5	1648	6	ADA83756	Ada83756 Human KIA
59	834	45.5	1648	8	ADQ15092	Adq15092 Human can
60	834	45.5	1648	8	ADU06498	Adu06498 Novel bro

ALIGNMENTS

RESULT 1
AAY06618
ID AAY06618 standard; protein; 784 AA.
XX
AC AAY06618;
XX
DT 26-OCT-1999 (first entry)
XX
DE Thermomyces lanuginosus kinesin motor protein TL-gamma.
XX
KW TL-gamma; kinesin; motor protein; microtubule; unc-104; infection;
KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; amyotrophic lateral sclerosis.
XX
OS Thermomyces lanuginosus.
XX
PN WO9937659-A1.
XX
PD 29-JUL-1999.
XX
PF 22-JAN-1999; 99WO-US001355.
XX
PR 23-JAN-1998; 98US-0072361P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Sakowicz R, Goldstein LSB;
XX
DR WPI; 1999-493950/41.
DR N-PSDB; AAX87656.
XX

```
PT   New nucleic acid encoding microtubule motor protein, used for diagnosis
PT   of fungal infection and neurodegenerative disease.
XX
PS   Claim 5; Page 70-71; 75pp; English.
XX
CC   This sequence represents Thermomyces lanuginosus TL-gamma, a novel ATP-
CC   dependent, plus end-directed microtubule motor protein that is a member
CC   of the unc-104 family and kinesin superfamily. The invention provides TL-
CC   gamma nucleic acids (see AAX87656), proteins and antibodies, and methods
CC   of screening for TL-gamma modulators potentially useful for treating
CC   hyphal fungal infections and diseases caused by mutated TL-gamma, e.g.
CC   neurodegeneration involving anterograde axonal transport, such as
CC   Alzheimer's, Parkinson's or Huntington's diseases or amyotrophic lateral
CC   sclerosis. Detection of TL-gamma allows differentiation between hyphal
CC   and non-hyphal fungal infections
XX
SQ   Sequence 784 AA;

  Query Match             100.0%;  Score 1834;  DB 2;  Length 784;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-172;
  Matches  357;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSGGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSGGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPK 60

Qy         61 AFAFDRSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AFAFDRSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120

Qy        121 YGKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YGKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180

Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240

Qy        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS 300

Qy        301 GKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK 357
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK 357


RESULT 2
AAM41820
ID   AAM41820 standard; protein; 421 AA.
XX
AC   AAM41820;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polypeptide SEQ ID NO 6751.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US034263.
XX
PR   23-DEC-1999;   99US-00471275.
PR   21-JAN-2000; 2000US-00488725.
PR   25-APR-2000; 2000US-00552317.
PR   20-JUN-2000; 2000US-00598042.
PR   19-JUL-2000; 2000US-00620312.
PR   03-AUG-2000; 2000US-00653450.
PR   14-SEP-2000; 2000US-00662191.
PR   19-OCT-2000; 2000US-00693036.
PR   29-NOV-2000; 2000US-00727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J,  Zhao QA;
PI   Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   N-PSDB; AAI60976.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders such
PT   as central nervous system injuries.
XX
PS   Example 2; SEQ ID NO 6751; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC   encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders. Note: The sequence data for this patent did not form
CC   part of the printed specification
XX
SQ   Sequence 421 AA;

  Query Match             62.8%;  Score 1152;  DB 4;  Length 421;
  Best Local Similarity   62.1%;  Pred. No. 8.8e-105;
  Matches  226;  Conservative   58;  Mismatches   56;  Indels   24;  Gaps    6;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||: | :|||::| |: | : |   :|           ||:|:
Db          9 GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET----------PKSPS 57

Qy         64 FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
              || ||||    :|   ||| |: :::|:|  :| :||:||| |||||||||:||||:|||
Db         58 FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG 115

Qy        121 YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
                 :  : |:||::|:|:| |||:   | |:: :|||||:||| |||||||||  ||||:|
Db        116 KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV 174

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
              ||||  |||||||:|| | |: :|::||| |||||||||||||||||||||||| :  |||
Db        175 REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK 234

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
              || || : ||||:|||||||||||||| |||| | |||||| ||:||:|||:||:|||:|
Db        235 RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM 294

Qy        299 SSG-----KQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYA 353
                      |:||   :||||||||||:::|||||  |||:||:|||||||::|||||||||
Db        295 DSGPNKNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYA 354

Qy        354 DSAK 357
              | ||
Db        355 DRAK 358
```

```
RESULT 3
ABM83651
ID   ABM83651 standard; protein; 1699 AA.
XX
AC   ABM83651;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:3900.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS   Homo sapiens.
XX
PN   WO2004023973-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Schmidt JP,  Wright RJ,  Bruns CM,  Marjanovic MM,  Shen F;
PI   Harthshorne TA,  Suchorolski MT,  Altus CM,  Pitts SJ,  Elder LV;
PI   Mooney EM,  Delegeane AM,  Panesar IS,  Banville SC,  Reddy TP;
PI   Stevens KA,  Blanchard JL,  Panzer SR,  Wang X,  Au AP,  Gerstin EH;
PI   Peralta CH,  Anderson SB,  Rioux P,  Shen EJ,  Wu MC,  Stuve LL;
PI   Lagace RE,  Spiro PA,  Stewart EA,  Wingrove J,  Vitt UA,  Kirton ES;
PI   Xu Y,  Kwong M,  Policky JL,  Hurwitz BL,  Ma Y,  Jackson JL,  Gietzen D;
PI   Patury S,  Shi X,  Suarez CJ;
XX
DR   WPI; 2004-329368/30.
DR   N-PSDB; ACN42303.
XX
PT   New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT   in gene mapping.
XX
PS   Claim 27; Page; 190pp; English.
XX
CC   The invention relates to novel diagnostic and therapeutic polynucleotides
CC   selected from one of the 2722 sequences defined in the specification. A
CC   polynucleotide of the invention may have a use in gene therapy. The human
CC   diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC   used to diagnose a particular condition, disease or disorder associated
CC   with human molecules, e.g. cell proliferative disorders,
CC   autoimmune/inflammatory disorder, developmental disorder, endocrine
CC   disorder, neurological disorders, gastrointestinal disorders, or
CC   infections caused by virus, bacteria, fungi or parasite. The dithp
CC   molecules may also be used in genetic mapping, in identifying individuals
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp protein of the
CC   invention. Note: The sequence data for this patent is not represented in
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 1699 AA;

  Query Match             62.8%;  Score 1152;  DB 8;  Length 1699;
  Best Local Similarity   62.1%;  Pred. No. 8.6e-104;
  Matches  226;  Conservative   58;  Mismatches   56;  Indels   24;  Gaps    6;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||: | :|||::| |: | :  |   :|            ||:|:
Db          3 GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET----------PKSFS 51

Qy         64 FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
                || ||||    :|   ||| |: :::|:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG 109

Qy        121 YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
                 :  : |:||::|:|:| |||:   | |:: :|||||:||| |||||||||  ||||:|
Db        110 KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV 168

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
              ||||  |||||||:|| | |: :|::||| |||||||||||||||||||||||||| :  |||
Db        169 REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK 228

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
              || || : ||||:|||||||||||||| |||| | |||||| ||:||:|||:||:|||:|
Db        229 RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM 288

Qy        299 SSG-----KQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYA 353
              ||      |:||   :|||||||||||:::||||| |||:||:||||||::|||||||||
Db        289 DSGPNKNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYA 348

Qy        354 DSAK 357
              | ||
Db        349 DRAK 352


RESULT 4
ABM83650
ID   ABM83650 standard; protein; 1708 AA.
XX
AC   ABM83650;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:3899.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS   Homo sapiens.
XX
PN   WO2004023973-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Schmidt JP,  Wright RJ,  Bruns CM,  Marjanovic MM,  Shen F;
PI   Harthshorne TA,  Suchorolski MT,  Altus CM,  Pitts SJ,  Elder LV;
PI   Mooney EM,  Delegeane AM,  Panesar IS,  Banville SC,  Reddy TP;
PI   Stevens KA,  Blanchard JL,  Panzer SR,  Wang X,  Au AP,  Gerstin EH;
PI   Peralta CH,  Anderson SB,  Rioux P,  Shen EJ,  Wu MC,  Stuve LL;
PI   Lagace RE,  Spiro PA,  Stewart EA,  Wingrove J,  Vitt UA,  Kirton ES;
PI   Xu Y,  Kwong M,  Policky JL,  Hurwitz BL,  Ma Y,  Jackson JL,  Gietzen D;
PI   Patury S,  Shi X,  Suarez CJ;
XX
DR   WPI; 2004-329368/30.
DR   N-PSDB; ACN42302.
XX
PT   New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT   in gene mapping.
XX
PS   Claim 27; Page; 190pp; English.
XX
CC   The invention relates to novel diagnostic and therapeutic polynucleotides
CC   selected from one of the 2722 sequences defined in the specification. A
CC   polynucleotide of the invention may have a use in gene therapy. The human
CC   diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC   used to diagnose a particular condition, disease or disorder associated
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```
CC   with human molecules, e.g. cell proliferative disorders,
CC   autoimmune/inflammatory disorder, developmental disorder, endocrine
CC   disorder, neurological disorders, gastrointestinal disorders, or
CC   infections caused by virus, bacteria, fungi or parasite. The dithp
CC   molecules may also be used in genetic mapping, in identifying individuals
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp protein of the
CC   invention. Note: The sequence data for this patent is not represented in
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 1708 AA;

  Query Match             62.8%;  Score 1152;  DB 8;  Length 1708;
  Best Local Similarity   62.1%;  Pred. No. 8.7e-104;
  Matches  226;  Conservative   58;  Mismatches   56;  Indels   24;  Gaps    6;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||: | :|||::| |: | :   |   :|            ||:|:
Db          3 GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET----------PKSFS 51

Qy         64 FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
              || ||||    :|   ||| |: :::|:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG 109

Qy        121 YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
               :  : |:||::|:|:| |||:   | |:: :|||||:||| |||||||||  ||||:|
Db        110 KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV 168

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
              ||||  |||||||:|| | |: :|::||| ||||||||||||||||||||||| :  |||
Db        169 REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK 228

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
              || || : ||||:|||||||||||||| |||| | |||||| ||:||:|||:||:|||:|
Db        229 RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM 288

Qy        299 SSG-----KQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYA 353
              ||     |:||   :|||||||||||:::||||| |||:||:|||||::|||||||||
Db        289 DSGPNKNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYA 348

Qy        354 DSAK 357
              | ||
Db        349 DRAK 352


RESULT 5
ABM83648
ID   ABM83648 standard; protein; 1714 AA.
XX
AC   ABM83648;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:3897.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS   Homo sapiens.
XX
PN   WO2004023973-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Schmidt JP,  Wright RJ,  Bruns CM,  Marjanovic MM,  Shen F;
PI   Harthshorne TA,  Suchorolski MT,  Altus CM,  Pitts SJ,  Elder LV;
PI   Mooney EM,  Delegeane AM,  Panesar IS,  Banville SC,  Reddy TP;
PI   Stevens KA,  Blanchard JL,  Panzer SR,  Wang X,  Au AP,  Gerstin EH;
PI   Peralta CH,  Anderson SB,  Rioux P,  Shen EJ,  Wu MC,  Stuve LL;
PI   Lagace RE,  Spiro PA,  Stewart EA,  Wingrove J,  Vitt UA,  Kirton ES;
PI   Xu Y,  Kwong M,  Policky JL,  Hurwitz BL,  Ma Y,  Jackson JL,  Gietzen D;
PI   Patury S,  Shi X,  Suarez CJ;
XX
DR   WPI; 2004-329368/30.
DR   N-PSDB; ACN42300.
XX
PT   New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT   in gene mapping.
XX
PS   Claim 27; Page; 190pp; English.
XX
CC   The invention relates to novel diagnostic and therapeutic polynucleotides
CC   selected from one of the 2722 sequences defined in the specification. A
CC   polynucleotide of the invention may have a use in gene therapy. The human
CC   diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC   used to diagnose a particular condition, disease or disorder associated
CC   with human molecules, e.g. cell proliferative disorders,
CC   autoimmune/inflammatory disorder, developmental disorder, endocrine
CC   disorder, neurological disorders, gastrointestinal disorders, or
CC   infections caused by virus, bacteria, fungi or parasite. The dithp
CC   molecules may also be used in genetic mapping, in identifying individuals
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp protein of the
CC   invention. Note: The sequence data for this patent is not represented in
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 1714 AA;

  Query Match             62.8%;  Score 1152;  DB 8;  Length 1714;
  Best Local Similarity   62.1%;  Pred. No. 8.7e-104;
  Matches  226;  Conservative   58;  Mismatches   56;  Indels   24;  Gaps    6;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||: | :|||::| |: | :   |   :|            ||:|:
Db          3 GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET----------PKSFS 51

Qy         64 FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
              || ||||    :|   ||| |: :::|:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG 109

Qy        121 YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
               :  : |:||::|:|:| |||:   | |:: :|||||:||| |||||||||  ||||:|
Db        110 KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV 168

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
              ||||  |||||||:|| | |: :|::||| ||||||||||||||||||||||| :  |||
Db        169 REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK 228

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
              || || : ||||:|||||||||||||| |||| | |||||| ||:||:|||:||:|||:|
Db        229 RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM 288

Qy        299 SSG-----KQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYA 353
              ||     |:||   :|||||||||||:::||||| |||:||:|||||::|||||||||
Db        289 DSGPNKNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYA 348

Qy        354 DSAK 357
              | ||
Db        349 DRAK 352


RESULT 6
ABM83647
ID   ABM83647 standard; protein; 1721 AA.
```

```
XX
AC   ABM83647;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:3896.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS   Homo sapiens.
XX
PN   WO2004023973-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Schmidt JP,  Wright RJ,  Bruns CM,  Marjanovic MM,  Shen F;
PI   Harthshorne TA,  Suchorolski MT,  Altus CM,  Pitts SJ,  Elder LV;
PI   Mooney EM,  Delegeane AM,  Panesar IS,  Banville SC,  Reddy TP;
PI   Stevens KA,  Blanchard JL,  Panzer SR,  Wang X,  Au AP,  Gerstin EH;
PI   Peralta CH,  Anderson SB,  Rioux P,  Shen EJ,  Wu MC,  Stuve LL;
PI   Lagace RE,  Spiro PA,  Stewart EA,  Wingrove J,  Vitt UA,  Kirton ES;
PI   Xu Y,  Kwong M,  Policky JL,  Hurwitz BL,  Ma Y,  Jackson JL,  Gietzen D;
PI   Patury S,  Shi X,  Suarez CJ;
XX
DR   WPI; 2004-329368/30.
DR   N-PSDB; ACN42299.
XX
PT   New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT   in gene mapping.
XX
PS   Claim 27; Page; 190pp; English.
XX
CC   The invention relates to novel diagnostic and therapeutic polynucleotides
CC   selected from one of the 2722 sequences defined in the specification. A
CC   polynucleotide of the invention may have a use in gene therapy. The human
CC   diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC   used to diagnose a particular condition, disease or disorder associated
CC   with human molecules, e.g. cell proliferative disorders,
CC   autoimmune/inflammatory disorder, developmental disorder, endocrine
CC   disorder, neurological disorders, gastrointestinal disorders, or
CC   infections caused by virus, bacteria, fungi or parasite. The dithp
CC   molecules may also be used in genetic mapping, in identifying individuals
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp protein of the
CC   invention. Note: The sequence data for this patent is not represented in
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 1721 AA;

  Query Match             62.8%;  Score 1152;  DB 8;  Length 1721;
  Best Local Similarity   62.1%;  Pred. No. 8.8e-104;
  Matches  226;  Conservative   58;  Mismatches   56;  Indels   24;  Gaps    6;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||: | :|||::| |: | :   |   :|            ||:|:
Db          3 GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET----------PKSFS 51

Qy         64 FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
                || ||||    :|   ||| |: :::|:|  :| :||:||| ||||||||:||||:|||
Db         52 FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG 109

Qy        121 YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
                :  : |:||::|:|:| |||:   | |:: :|||||:||| |||||||||  ||||:|
Db        110 KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV 168

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
              ||||  |||||||:|| | |: :|::||| |||||||||||||||||||||| :  |||
Db        169 REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK 228

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
              || || : ||||:||||||||||||| |||| | |||||| ||:||:|||:||:|||:|
Db        229 RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM 288

Qy        299 SSG-----KQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYA 353
                 ||      |:||   :|||||||||||:::||||| |||:||:||||||::|||||||||
Db        289 DSGPNKNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYA 348

Qy        354 DSAK 357
              | ||
Db        349 DRAK 352


RESULT 7
AAM40034
ID   AAM40034 standard; protein; 893 AA.
XX
AC   AAM40034;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polypeptide SEQ ID NO 3179.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US034263.
XX
PR   23-DEC-1999;   99US-00471275.
PR   21-JAN-2000; 2000US-00488725.
PR   25-APR-2000; 2000US-00552317.
PR   20-JUN-2000; 2000US-00598042.
PR   19-JUL-2000; 2000US-00620312.
PR   03-AUG-2000; 2000US-00653450.
PR   14-SEP-2000; 2000US-00662191.
PR   19-OCT-2000; 2000US-00693036.
PR   29-NOV-2000; 2000US-00727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J,  Zhao QA;
PI   Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   N-PSDB; AAI59190.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders such
PT   as central nervous system injuries.
XX
PS   Example 4; SEQ ID NO 3179; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC   encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
```

```
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders. Note: The sequence data for this patent did not form
CC   part of the printed specification
XX
SQ   Sequence 893 AA;

  Query Match             62.6%;  Score 1149;  DB 4;  Length 893;
  Best Local Similarity   61.8%;  Pred. No. 6e-104;
  Matches  225;  Conservative   59;  Mismatches   56;  Indels   24;  Gaps    6;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||: | :|||::| |: | :  |   :|            ||:|:
Db          3 GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET----------PKSFS 51

Qy         64 FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
              || |||:    :|   ||| |: :::|:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWA--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG 109

Qy        121 YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
               :  : |:||::|:|:| |||:   | |:: :|||||:||| |||||||||  ||||:|
Db        110 KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV 168

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
              ||||  |||||||:|| | |: :|::||| |||||||||||||||||||||||| :  |||
Db        169 REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK 228

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
              || || : ||||:|||||||||||||| |||| | |||||| ||:||:|||:||:|||:|
Db        229 RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM 288

Qy        299 SSG-----KQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYA 353
              ||     |:||   :|||||||||||:::||||| |||:||:||||||::|||||||||
Db        289 DSGPNKNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYA 348

Qy        354 DSAK 357
              | ||
Db        349 DRAK 352


RESULT 8
ABM83653
ID   ABM83653 standard; protein; 1696 AA.
XX
AC   ABM83653;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:3902.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS   Homo sapiens.
XX
PN   WO2004023973-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Schmidt JP,  Wright RJ,  Bruns CM,  Marjanovic MM,  Shen F;
PI   Harthshorne TA,  Suchorolski MT,  Altus CM,  Pitts SJ,  Elder LV;
PI   Mooney EM,  Delegeane AM,  Panesar IS,  Banville SC,  Reddy TP;
PI   Stevens KA,  Blanchard JL,  Panzer SR,  Wang X,  Au AP,  Gerstin EH;
PI   Peralta CH,  Anderson SB,  Rioux P,  Shen EJ,  Wu MC,  Stuve LL;
PI   Lagace RE,  Spiro PA,  Stewart EA,  Wingrove J,  Vitt UA,  Kirton ES;
PI   Xu Y,  Kwong M,  Policky JL,  Hurwitz BL,  Ma Y,  Jackson JL,  Gietzen D;
PI   Patury S,  Shi X,  Suarez CJ;
XX
DR   WPI; 2004-329368/30.
DR   N-PSDB; ACN42305.
XX
PT   New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT   in gene mapping.
XX
PS   Claim 27; Page; 190pp; English.
XX
CC   The invention relates to novel diagnostic and therapeutic polynucleotides
CC   selected from one of the 2722 sequences defined in the specification. A
CC   polynucleotide of the invention may have a use in gene therapy. The human
CC   diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC   used to diagnose a particular condition, disease or disorder associated
CC   with human molecules, e.g. cell proliferative disorders,
CC   autoimmune/inflammatory disorder, developmental disorder, endocrine
CC   disorder, neurological disorders, gastrointestinal disorders, or
CC   infections caused by virus, bacteria, fungi or parasite. The dithp
CC   molecules may also be used in genetic mapping, in identifying individuals
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp protein of the
CC   invention. Note: The sequence data for this patent is not represented in
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 1696 AA;

  Query Match             62.3%;  Score 1142;  DB 8;  Length 1696;
  Best Local Similarity   61.9%;  Pred. No. 8.4e-103;
  Matches  224;  Conservative   59;  Mismatches   57;  Indels   22;  Gaps    6;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||: | :|||::| |: | :  |   :|            ||:|:
Db          3 GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET----------PKSFS 51

Qy         64 FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
              || ||||    :|   ||| |: :::|:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG 109

Qy        121 YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
               :  : |:||::|:|:| |||:   | |:: :|||||:||| |||||||||  ||||:|
Db        110 KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV 168

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
              ||||  |||||||:|| | |: :|::||| |||||||||||||||||||||||| :  |||
Db        169 REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK 228

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
              || || : ||||:|||||||||||||| |||| | |||||| ||:||:|||:||:|||:|
Db        229 RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM 288

Qy        299 ---SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADS 355
                   : |:||   :|||||||||||:::||||| |||:||:||||||::||||||||||
Db        289 XPPQNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADR 348

Qy        356 AK 357
              ||
Db        349 AK 350


RESULT 9
ABM83652
ID   ABM83652 standard; protein; 1697 AA.
```

```
XX
AC   ABM83652;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:3901.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS   Homo sapiens.
XX
PN   WO2004023973-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
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PI   Harthshorne TA,  Suchorolski MT,  Altus CM,  Pitts SJ,  Elder LV;
PI   Mooney EM,  Delegeane AM,  Panesar IS,  Banville SC,  Reddy TP;
PI   Stevens KA,  Blanchard JL,  Panzer SR,  Wang X,  Au AP,  Gerstin EH;
PI   Peralta CH,  Anderson SB,  Rioux P,  Shen EJ,  Wu MC,  Stuve LL;
PI   Lagace RE,  Spiro PA,  Stewart EA,  Wingrove J,  Vitt UA,  Kirton ES;
PI   Xu Y,  Kwong M,  Policky JL,  Hurwitz BL,  Ma Y,  Jackson JL,  Gietzen D;
PI   Patury S,  Shi X,  Suarez CJ;
XX
DR   WPI; 2004-329368/30.
DR   N-PSDB; ACN42304.
XX
PT   New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT   in gene mapping.
XX
PS   Claim 27; Page; 190pp; English.
XX
CC   The invention relates to novel diagnostic and therapeutic polynucleotides
CC   selected from one of the 2722 sequences defined in the specification. A
CC   polynucleotide of the invention may have a use in gene therapy. The human
CC   diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC   used to diagnose a particular condition, disease or disorder associated
CC   with human molecules, e.g. cell proliferative disorders,
CC   autoimmune/inflammatory disorder, developmental disorder, endocrine
CC   disorder, neurological disorders, gastrointestinal disorders, or
CC   infections caused by virus, bacteria, fungi or parasite. The dithp
CC   molecules may also be used in genetic mapping, in identifying individuals
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp protein of the
CC   invention. Note: The sequence data for this patent is not represented in
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 1697 AA;

  Query Match           62.3%;  Score 1142;  DB 8;  Length 1697;
  Best Local Similarity  61.9%;  Pred. No. 8.4e-103;
  Matches  224;  Conservative   59;  Mismatches   57;  Indels   22;  Gaps    6;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||: | :|||::| |: | :   |   :|           ||:|:
Db          3 GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET----------PKSFS 51

Qy         64 FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
                || ||||    :|   ||| |: :::|:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG 109

Qy        121 YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
```

```
                :  : |:||::|:|:| |||:   | |:: :|||||:||| |||||||||  ||||:|
Db        110 KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV 168

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
              ||||  |||||||:|| | |: :|::||| |||||||||||||||||||||||| :  |||
Db        169 REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK 228

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
               || || : ||||:|||||||||||||| |||| | |||||| ||:||:|||:||:|||:|
Db        229 RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM 288

Qy        299 ---SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADS 355
                  : |:||   :|||||||||||:::||||| |||:||:||||||::||||||||||
Db        289 XPPQNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADR 348

Qy        356 AK 357
              ||
Db        349 AK 350
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RESULT 10
ABM83649
ID   ABM83649 standard; protein; 1709 AA.
XX
AC   ABM83649;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:3898.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS   Homo sapiens.
XX
PN   WO2004023973-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Schmidt JP,  Wright RJ,  Bruns CM,  Marjanovic MM,  Shen F;
PI   Harthshorne TA,  Suchorolski MT,  Altus CM,  Pitts SJ,  Elder LV;
PI   Mooney EM,  Delegeane AM,  Panesar IS,  Banville SC,  Reddy TP;
PI   Stevens KA,  Blanchard JL,  Panzer SR,  Wang X,  Au AP,  Gerstin EH;
PI   Peralta CH,  Anderson SB,  Rioux P,  Shen EJ,  Wu MC,  Stuve LL;
PI   Lagace RE,  Spiro PA,  Stewart EA,  Wingrove J,  Vitt UA,  Kirton ES;
PI   Xu Y,  Kwong M,  Policky JL,  Hurwitz BL,  Ma Y,  Jackson JL,  Gietzen D;
PI   Patury S,  Shi X,  Suarez CJ;
XX
DR   WPI; 2004-329368/30.
DR   N-PSDB; ACN42301.
XX
PT   New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT   in gene mapping.
XX
PS   Claim 27; Page; 190pp; English.
XX
CC   The invention relates to novel diagnostic and therapeutic polynucleotides
CC   selected from one of the 2722 sequences defined in the specification. A
CC   polynucleotide of the invention may have a use in gene therapy. The human
CC   diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC   used to diagnose a particular condition, disease or disorder associated
CC   with human molecules, e.g. cell proliferative disorders,
CC   autoimmune/inflammatory disorder, developmental disorder, endocrine
CC   disorder, neurological disorders, gastrointestinal disorders, or
CC   infections caused by virus, bacteria, fungi or parasite. The dithp
```

```
CC   molecules may also be used in genetic mapping, in identifying individuals
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp protein of the
CC   invention. Note: The sequence data for this patent is not represented in
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 1709 AA;

  Query Match             62.3%;  Score 1142;  DB 8;  Length 1709;
  Best Local Similarity   61.9%;  Pred. No. 8.5e-103;
  Matches  224;  Conservative   59;  Mismatches   57;  Indels   22;  Gaps    6;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||: | :|||::| |: | :  |   :|            ||:|:
Db          3 GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET----------PKSFS 51

Qy         64 FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
              || ||||    :|   ||| |: :::|:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG 109

Qy        121 YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
               :  : |:||::|:|:| |||:   | |:: :|||||:||| |||||||||  ||||:|
Db        110 KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV 168

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
              ||||  |||||||:|| | |: :|::||| ||||||||||||||||||||||||| :  |||
Db        169 REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK 228

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
              || || : ||||:|||||||||||| |||| | |||||| ||:||:|||:||:|||:|
Db        229 RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM 288

Qy        299 ---SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADS 355
                 : |:||   :|||||||||||:::||||| |||:||:||||||::||||||||||
Db        289 XPPQNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADR 348

Qy        356 AK 357
              ||
Db        349 AK 350


RESULT 11
ABM83646
ID   ABM83646 standard; protein; 1722 AA.
XX
AC   ABM83646;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:3895.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS   Homo sapiens.
XX
PN   WO2004023973-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Schmidt JP,  Wright RJ,  Bruns CM,  Marjanovic MM,  Shen F;
PI   Harthshorne TA,  Suchorolski MT,  Altus CM,  Pitts SJ,  Elder LV;
PI   Mooney EM,  Delegeane AM,  Panesar IS,  Banville SC,  Reddy TP;
PI   Stevens KA,  Blanchard JL,  Panzer SR,  Wang X,  Au AP,  Gerstin EH;
PI   Peralta CH,  Anderson SB,  Rioux P,  Shen EJ,  Wu MC,  Stuve LL;
PI   Lagace RE,  Spiro PA,  Stewart EA,  Wingrove J,  Vitt UA,  Kirton ES;
PI   Xu Y,  Kwong M,  Policky JL,  Hurwitz BL,  Ma Y,  Jackson JL,  Gietzen D;
PI   Patury S,  Shi X,  Suarez CJ;
XX
DR   WPI; 2004-329368/30.
DR   N-PSDB; ACN42298.
XX
PT   New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT   in gene mapping.
XX
PS   Claim 27; Page; 190pp; English.
XX
CC   The invention relates to novel diagnostic and therapeutic polynucleotides
CC   selected from one of the 2722 sequences defined in the specification. A
CC   polynucleotide of the invention may have a use in gene therapy. The human
CC   diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC   used to diagnose a particular condition, disease or disorder associated
CC   with human molecules, e.g. cell proliferative disorders,
CC   autoimmune/inflammatory disorder, developmental disorder, endocrine
CC   disorder, neurological disorders, gastrointestinal disorders, or
CC   infections caused by virus, bacteria, fungi or parasite. The dithp
CC   molecules may also be used in genetic mapping, in identifying individuals
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp protein of the
CC   invention. Note: The sequence data for this patent is not represented in
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 1722 AA;

  Query Match             62.3%;  Score 1142;  DB 8;  Length 1722;
  Best Local Similarity   61.9%;  Pred. No. 8.6e-103;
  Matches  224;  Conservative   59;  Mismatches   57;  Indels   22;  Gaps    6;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||: | :|||::| |: | :  |   :|            ||:|:
Db          3 GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET----------PKSFS 51

Qy         64 FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
              || ||||    :|   ||| |: :::|:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG 109

Qy        121 YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
               :  : |:||::|:|:| |||:   | |:: :|||||:||| |||||||||  ||||:|
Db        110 KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV 168

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
              ||||  |||||||:|| | |: :|::||| ||||||||||||||||||||||||| :  |||
Db        169 REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK 228

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
              || || : ||||:|||||||||||| |||| | |||||| ||:||:|||:||:|||:|
Db        229 RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM 288

Qy        299 ---SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADS 355
                 : |:||   :|||||||||||:::||||| |||:||:||||||::||||||||||
Db        289 XPPQNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADR 348

Qy        356 AK 357
              ||
Db        349 AK 350


RESULT 12
ABM83671
ID   ABM83671 standard; protein; 1199 AA.
XX
AC   ABM83671;
XX
DT   18-NOV-2004  (first entry)
```

```
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:3920.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS   Homo sapiens.
XX
PN   WO2004023973-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Schmidt JP,  Wright RJ,  Bruns CM,  Marjanovic MM,  Shen F;
PI   Harthshorne TA,  Suchorolski MT,  Altus CM,  Pitts SJ,  Elder LV;
PI   Mooney EM,  Delegeane AM,  Panesar IS,  Banville SC,  Reddy TP;
PI   Stevens KA,  Blanchard JL,  Panzer SR,  Wang X,  Au AP,  Gerstin EH;
PI   Peralta CH,  Anderson SB,  Rioux P,  Shen EJ,  Wu MC,  Stuve LL;
PI   Lagace RE,  Spiro PA,  Stewart EA,  Wingrove J,  Vitt UA,  Kirton ES;
PI   Xu Y,  Kwong M,  Policky JL,  Hurwitz BL,  Ma Y,  Jackson JL,  Gietzen D;
PI   Patury S,  Shi X,  Suarez CJ;
XX
DR   WPI; 2004-329368/30.
DR   N-PSDB; ACN42323.
XX
PT   New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT   in gene mapping.
XX
PS   Claim 27; Page; 190pp; English.
XX
CC   The invention relates to novel diagnostic and therapeutic polynucleotides
CC   selected from one of the 2722 sequences defined in the specification. A
CC   polynucleotide of the invention may have a use in gene therapy. The human
CC   diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC   used to diagnose a particular condition, disease or disorder associated
CC   with human molecules, e.g. cell proliferative disorders,
CC   autoimmune/inflammatory disorder, developmental disorder, endocrine
CC   disorder, neurological disorders, gastrointestinal disorders, or
CC   infections caused by virus, bacteria, fungi or parasite. The dithp
CC   molecules may also be used in genetic mapping, in identifying individuals
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp protein of the
CC   invention. Note: The sequence data for this patent is not represented in
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 1199 AA;

  Query Match             61.0%;  Score 1119;  DB 8;  Length 1199;
  Best Local Similarity   60.8%;  Pred. No. 9.1e-101;
  Matches  220;  Conservative   59;  Mismatches   63;  Indels   20;  Gaps    5;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||  : :|||::|:|| | :  |   :|           ||:|:
Db          3 GASVKVAVRVRPFNSRETSKESKCIIQMQGNSTSIINPKNPKE----------APKSFS 51

Qy         64 FDRSYWSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122
              || ||||     | :| |  :: |:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWSHTSPEDPCFASQNRVYNDIGKEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGKQ 111

Qy        123 KEH--GVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
              :|   |:||::|:::| :||:   :: :: :|||||:||| |||||||||  ||||:|||
Db        112 EESQAGIIPQLCEELFEKIND-NCNEEMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE 170

Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240
              || |||||||:|| | |: :| :||| ||||||||||||||||||||||:  ||| |
Db        171 HPLLGPYVEDLSKLAVTSYTDIADLMDAGNKARTVAATNMNETSSRSHAVFTIVFTQKKH 230

Qy        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM-- 298
              | || : ||||:|||||||||||||| |||| | |||||| ||:||:|||:||:|||::
Db        231 DNETNLSTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEVDN 290

Qy        299 ---SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADS 355
                  | |:||   :||||||||||:::||||| |||:||:|||||::||||||||||
Db        291 CTSKSKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADR 350

Qy        356 AK 357
              ||
Db        351 AK 352


RESULT 13
AAB36227
ID   AAB36227 standard; protein; 1816 AA.
XX
AC   AAB36227;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Human kinesin-like protein HKLP SEQ ID NO: 4.
XX
KW   Human; kinesin-like protein; HKLP; KIF1; cell division; cancer;
KW   intracellular transport; neurological disorder; infertility;
KW   biallelic marker; spontaneous abortion; neonatal chromosome disorder;
KW   aneuploidy.
XX
OS   Homo sapiens.
XX
PN   WO200063375-A1.
XX
PD   26-OCT-2000.
XX
PF   20-APR-2000; 2000WO-IB000562.
XX
PR   20-APR-1999;   99US-0130217P.
XX
PA   (GEST.) GENSET.
XX
PI   Bougueleret L,  Dufaure-Gare I,  Grel P;
XX
DR   WPI; 2000-665242/64.
DR   N-PSDB; AAC66550.
XX
PT   An isolated or purified human kinesin-like protein (HKLP) encoding
PT   polynucleotide used to detect HKLP polynucleotides in a sample comprises
PT   a contiguous span of at least 12 nucleotides.
XX
PS   Claim 46; Page 189-192; 199pp; English.
XX
CC   The present invention describes the coding and protein sequences of the
CC   human kinesin-like protein HKLP. It is thought that the protein could be
CC   involved in neurological disorders, infertility, spontaneous abortion,
CC   neonatal chromosome disorders, aneuploidy and cancers. This is due to its
CC   function in the movement of microtubules. The protein shows homology to
CC   the murine KIF1A and KIF1B proteins. The sequences disclosed in the
CC   invention can be used in the isolation of similar human proteins and in
CC   vector production. In addition, the biallelic markers shown can be used
CC   in disease diagnosis and population studies
XX
SQ   Sequence 1816 AA;

  Query Match             61.0%;  Score 1119;  DB 3;  Length 1816;
  Best Local Similarity   60.8%;  Pred. No. 1.8e-100;
  Matches  220;  Conservative   59;  Mismatches   63;  Indels   20;  Gaps    5;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||  : :|||::|:|| | :  |   :|           ||:|:
Db          3 GASVKVAVRVRPFNSRETSKESKCIIQMQGNSTSIINPKNPKE----------APKSFS 51
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```
Qy         64 FDRSYWSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122
              || ||||      | :| |  :: |:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWSHTSPEDPCFASQNRVYNDIGKEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGKQ 111

Qy        123 KEH--GVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
              :|   |:||::|:::| :||:   :: :: :|||||:||| |||||||||  ||||:|||
Db        112 EESQAGIIPQLCEELFEKIND-NCNEEMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE 170

Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240
              ||  |||||||:|| | |: :| :||| ||||||||||||||||||||||:  ||| |
Db        171 HPLLGPYVEDLSKLAVTSYTDIADLMDAGNKARTVAATNMNETSSRSHAVFTIVFTQKKH 230

Qy        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM-- 298
              | || : ||||:|||||||||||||| |||| | |||||| ||:||:|||:||:|||::
Db        231 DNETNLSTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEVDN 290

Qy        299 ---SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADS 355
                 | |:||   :||||||||||:::||||| |||:||:||||||::||||||||||
Db        291 CTSKSKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADR 350

Qy        356 AK 357
              ||
Db        351 AK 352
```

RESULT 14
ABB07867
ID ABB07867 standard; protein; 1823 AA.
XX
AC ABB07867;
XX
DT 03-JUL-2002 (first entry)
XX
DE Human kinesin-associated protein having motor domain.
XX
KW Human; kinesin-associated protein; motor domain; cytostatic; KIF1B-beta;
KW neuroblastoma.
XX
OS Homo sapiens.
XX
PN WO200226965-A1.
XX
PD 04-APR-2002.
XX
PF 01-OCT-2001; 2001WO-JP008635.
XX
PR 29-SEP-2000; 2000JP-00300247.
XX
PA (HISM) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
XX
PI Nakagawara A;
XX
DR WPI; 2002-340013/37.
DR N-PSDB; ABL40908.
XX
PT Gene encoding human kinesin-associated protein with motor domain, useful
PT for diagnosis and treatment of neuroblastoma.
XX
PS Claim 2; Page 40-48; 57pp; Japanese.
XX
CC The invention provides a human kinesin-associated gene encoding a protein
CC having a motor domain and another protein encoded by the human kinesin-
CC associated gene having no motor domain. The genes are useful for the
CC diagnosis and treatment of human neuroblastoma, and judgement of
CC prognosis of this disease. Also provided are probes and primers
CC hybridising to part of the KIF1B-beta gene, useful for diagnosing
CC neuroblastoma in which the gene sequence is detected in tissue samples.
CC The present sequence represents a human kinesin-associated protein having
CC the motor domain
XX
SQ Sequence 1823 AA;

Query Match 61.0%; Score 1119; DB 5; Length 1823;
Best Local Similarity 60.8%; Pred. No. 1.8e-100;
Matches 220; Conservative 59; Mismatches 63; Indels 20; Gaps 5;

```
Qy          4 GGNIKVVVRVRPFNARE IDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||  : :|||::|:|| | :  |   :|           ||:|:
Db          3 GASVKVAVRVRPFNSRETSKESKCIIQMQGNSTSIINPKNPKE----------APKSFS 51

Qy         64 FDRSYWSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122
              || ||||      | :| |  :: |:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWSHTSPEDPCFASQNRVYNDIGKEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGKQ 111

Qy        123 KEH--GVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
              :|   |:||::|:::| :||:   :: :: :|||||:||| |||||||||  ||||:|||
Db        112 EESQAGIIPQLCEELFEKIND-NCNEEMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE 170

Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240
              ||  |||||||:|| | |: :| :||| ||||||||||||||||||||||:  ||| |
Db        171 HPLLGPYVEDLSKLAVTSYTDIADLMDAGNKARTVAATNMNETSSRSHAVFTIVFTQKKH 230

Qy        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM-- 298
              | || : ||||:|||||||||||||| |||| | |||||| ||:||:|||:||:|||::
Db        231 DNETNLSTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEVDN 290

Qy        299 ---SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADS 355
                 | |:||   :||||||||||:::||||| |||:||:||||||::||||||||||
Db        291 CTSKSKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADR 350

Qy        356 AK 357
              ||
Db        351 AK 352
```

RESULT 15
AAY51328
ID AAY51328 standard; protein; 1103 AA.
XX
AC AAY51328;
XX
DT 17-APR-2000 (first entry)
XX
DE Human KLIMP protein.
XX
KW KLIMP; kinesin-like motor protein; cytostatic; anticonvulsant; human;
KW anti-Alzheimer; anti-Parkinsonian; antidiabetic; anti-ulcerative; cancer;
KW immunomodulatory; antiinflammatory; anti-AIDS; antirheumatic; treatment;
KW antiarthritic; diagnosis; neurological disorder; vesicular transport.
XX
OS Homo sapiens.
XX
PN US6013454-A.
XX
PD 11-JAN-2000.
XX
PF 28-SEP-1998; 98US-00162373.
XX
PR 28-SEP-1998; 98US-00162373.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Tang YT, Corley NC, Patterson C, Guegler KJ;
XX
DR WPI; 2000-126064/11.
DR N-PSDB; AAZ44744.
XX
PT Nucleic acid sequences encoding a human kinesin-like motor protein
PT (KLIMP) useful for the treatment of diseases associated with
PT inappropriate KLIMP expression such as cancers, neurological disorders
PT and disorders of vesicular transport.
XX
PS Claim 1; Fig 1A-J; 38pp; English.
XX

```
CC   This invention describes a novel human kinesin-like motor protein (KLIMP)
CC   (I) which has cytostatic, anticonvulsant, anti-Alzheimer's, anti-
CC   Parkinsonian, antidiabetic, anti-ulcerative, immunomodulatory,
CC   antiinflammatory, anti-AIDS, antirheumatic and antiarthritic activity.
CC   (I) and the protein it encodes may be used in the prevention, treatment
CC   and diagnosis of diseases associated with inappropriate KLIMP expression
CC   such as cancers, neurological disorders and disorders of vesicular
CC   transport. For example, (I) (and vectors containing (I) (Iv)) and the
CC   KLIMP polypeptide may be used to treat disorders associated with
CC   decreased KLIMP expression such as cancers (e.g. lymphoma, melanoma and
CC   cancers of the breast lung and prostate), neurological disorders (e.g.
CC   epilepsy, Alzheimer's disease and Parkinson's disease), disorders of
CC   vesicular transport (e.g. diabetes mellitus/insipidus, Grave's disease
CC   and gastric/duodenal ulcers), and some immune/inflammatory diseases (e.g.
CC   acquired immune deficiency syndrome AIDS), rheumatoid arthritis and toxic
CC   shock syndrome). This sequence represents the human KLIMP protein
CC   described in the method of the invention
XX
SQ   Sequence 1103 AA;

  Query Match             60.9%;  Score 1117;  DB 3;  Length 1103;
  Best Local Similarity   61.6%;  Pred. No. 1.3e-100;
  Matches  220;  Conservative   59;  Mismatches   62;  Indels   16;  Gaps    5;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||||  : |||:| |:|| | :  |           |   | ||:|
Db          3 GASVKVAVRVRPFNARETSQDAKCVVSMQGNTTSIINP----------KQSKDAPKSFT 51

Qy         64 FDRSYWSFDKNA-PNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122
              || ||||      | :| |: :::|:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWSHTSTEDPQFASQQQVYRDIGEEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGRQ 111

Qy        123 K--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
              :  : |::|::|:|:| |::| |    |: :|||||:||| ||||||||| ::|:|:|||
Db        112 EPGQQGIVPQLCEDLFSRVSENQ-SAQLSYSVEVSYMEIYCERVRDLLNPKSRGSLRVRE 170

Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240
              ||  ||||:||:|| | |: :| :||| |||||||||||||||||||||:  ||: |
Db        171 HPILGPYVQDLSKLAVTSYADIADLMDCGNKARTVAATNMNETSSRSHAVFTIVFTQRCH 230

Qy        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS 300
              |: | :|:|||:|||||||||||| |:|| |  ||||| ||:||:|||:||:||||| |
Db        231 DQLTGLDSEKVSKISLVDLAGSERADSSGARGMGLKEGANINKSLTTLGKVISALADMQS 290

Qy        301 GKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK 357
               |::|:  :|||||||||||::|||| |||||:||||||:||||||||||  |
Db        291 -KKRKSDFIPYRDSVLTWLLKENLGGNSRTAMIAALSPADINYEETLSTLRYADRTK 346


RESULT 16
AAE04316
ID   AAE04316 standard; protein; 1103 AA.
XX
AC   AAE04316;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human kinesin-like motor protein (KLIMP).
XX
KW   Human; kinesin-like motor protein; KLIMP; cancer; adenocarcinoma;
KW   leukaemia; lymphoma; melanoma; neurological disorder; epilepsy;
KW   ischaemic cerebrovascular disease; stroke; Alzheimer's disease;
KW   Pick's disease; Huntington's disease; dementia; Parkinson's disease;
KW   vesicular transport disorder; cystic fibrosis; diabetes mellitus; AIDS;
KW   Acquired Immune Deficiency Syndrome; microbial infection.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          11. .377
FT                   /label= Kinesin_motor_domain
FT                   /note= "This region is specifically referred in claim 1"
FT   Binding-site    97. .104
FT                   /note= "ATP-binding site"
FT   Region          242. .253
FT                   /note= "Kinesin motor domain signature"
XX
PN   US6248594-B1.
XX
PD   19-JUN-2001.
XX
PF   21-DEC-1999;   99US-00467946.
XX
PR   28-SEP-1998;   98US-00162373.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Tang YT,  Corley NC,  Guegler KJ,  Patterson C;
XX
DR   WPI; 2001-407322/43.
DR   N-PSDB; AAD08139.
XX
PT   Nucleic acid sequences encoding a human kinesin-like motor protein
PT   (KLIMP) useful for the prevention and treatment of diseases associated
PT   with inappropriate KLIMP expression such as cancers and neurological
PT   disorders.
XX
PS   Claim 1; Fig 1; 37pp; English.
XX
CC   The present sequence is human kinesin-like motor protein (KLIMP) from
CC   Incyte clone 1281811. KLIMP and the corresponding polynucleotide are
CC   useful for diagnosis, treatment and prevention of disorders associated
CC   with decreased expression of KLIMP e.g. cancers (such as adenocarcinoma,
CC   leukaemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in
CC   particular, cancers of the adrenal gland), neurological disorders (such
CC   as epilepsy, ischaemic cerebrovascular disease, stroke, cerebral
CC   neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease,
CC   dementia, Parkinson's disease, peripheral nervous system disorders,
CC   mental disorders), and disorders of vesicular transport (such as cystic
CC   fibrosis, diabetes mellitus, AIDS (Acquired Immune Deficiency Syndrome),
CC   viral, bacterial, fungal, helminthic, and protozoal infections)
XX
SQ   Sequence 1103 AA;

  Query Match             60.9%;  Score 1117;  DB 4;  Length 1103;
  Best Local Similarity   61.6%;  Pred. No. 1.3e-100;
  Matches  220;  Conservative   59;  Mismatches   62;  Indels   16;  Gaps    5;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||||  : |||:| |:|| | :  |           |   | ||:|
Db          3 GASVKVAVRVRPFNARETSQDAKCVVSMQGNTTSIINP----------KQSKDAPKSFT 51

Qy         64 FDRSYWSFDKNA-PNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122
              || ||||      | :| |: :::|:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWSHTSTEDPQFASQQQVYRDIGEEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGRQ 111

Qy        123 K--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
              :  : |::|::|:|:| |::| |    |: :|||||:||| ||||||||| ::|:|:|||
Db        112 EPGQQGIVPQLCEDLFSRVSENQ-SAQLSYSVEVSYMEIYCERVRDLLNPKSRGSLRVRE 170

Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240
              ||  ||||:||:|| | |: :| :||| |||||||||||||||||||||:  ||: |
Db        171 HPILGPYVQDLSKLAVTSYADIADLMDCGNKARTVAATNMNETSSRSHAVFTIVFTQRCH 230

Qy        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS 300
              |: | :|:|||:|||||||||||| |:|| |  ||||| ||:||:|||:||:||||| |
Db        231 DQLTGLDSEKVSKISLVDLAGSERADSSGARGMGLKEGANINKSLTTLGKVISALADMQS 290

Qy        301 GKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK 357
               |::|:  :|||||||||||::|||| |||||:||||||:||||||||||  |
Db        291 -KKRKSDFIPYRDSVLTWLLKENLGGNSRTAMIAALSPADINYEETLSTLRYADRTK 346


RESULT 17
ABG72054
ID   ABG72054 standard; protein; 1103 AA.
```

```
XX
AC   ABG72054;
XX
DT   31-JAN-2003  (first entry)
XX
DE   Human kinesin-like motor protein, KLIMP.
XX
KW   Human; kinesin-like motor protein; KLIMP; kinesin;
KW   microtuble motor protein; ATPase; force; directional movement; agonist;
KW   antagonist; diagnostic; transgenic; gene therapy; cancer;
KW   neurological disorder; Alzheimer's disease; Parkinson's disease;
KW   dementia; epilepsy; vesicular transport; cystic fibrosis;
KW   hypercholesterolaemia; diabetes mellitus; hyperglycaemia; hypoglycaemia;
KW   gastrointestinal disorder; ulcerative colitis;
KW   acquired immunodeficiency syndrome; AIDS; allergy; multiple sclerosis;
KW   rheumatoid arthritis; infection; human immunodeficiency virus.
XX
OS   Homo sapiens.
XX
PN   US2002127668-A1.
XX
PD   12-SEP-2002.
XX
PF   02-MAY-2001; 2001US-00847874.
XX
PR   28-SEP-1998;   98US-00162373.
PR   21-DEC-1999;   99US-00467946.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Tang YT,  Corley NC,  Guegler KJ,  Patterson C;
XX
DR   WPI; 2003-066902/06.
DR   N-PSDB; ABS57217.
XX
PT   Novel human kinesin-like motor protein, useful in diagnosis, prevention
PT   and treatment of cancer, neurological disorders, and disorders associated
PT   with vesicular transport.
XX
PS   Claim 1; Fig 1; 41pp; English.
XX
CC   The invention discloses an isolated human kinesin-like motor protein
CC   (KLIMP), and the polynucleotide encoding it. Kinesins are microtubule
CC   motor proteins which have an activity that includes microtubule
CC   stimulated ATPase activity which generates force and directional
CC   movement. The KLIMP protein is useful for screening a compound for
CC   effectiveness as an agonist or antagonist, for screening a compound that
CC   specifically binds KLIMP or modulates its activity and for preparing a
CC   polyclonal or monoclonal antibody by hybridoma technology. The
CC   polynucleotide, polypeptide, antibody and compounds are useful for
CC   screening a compound for effectiveness in altering expression of a KLIMP,
CC   for assessing toxicity of a test compound, in a diagnostic test for a
CC   condition or a disease associated with the expression of KLIMP, for
CC   detecting KLIMP in a sample and for purifying KLIMP. They are also useful
CC   for creating knockin humanised animals or transgenic animals to model
CC   human diseases and in somatic or germline gene therapy. The diseases or
CC   conditions associated with a modulated expression of functional KLIMP are
CC   cancer, a neurological disorder (e.g. Alzheimer's disease, Parkinson's
CC   disease, dementia, depression, epilepsy and stroke), a disorder of the
CC   vesicular transport (e.g. cystic fibrosis, hypercholesterolaemia,
CC   diabetes mellitus, hyper- and hypoglycaemia, Grave's disease, goiter,
CC   gastrointestinal disorders such as ulcerative colitis, other conditions
CC   associated with abnormal vesicle trafficking such as acquired
CC   immunodeficiency syndrome (AIDS), allergic reactions, multiple sclerosis,
CC   rheumatoid arthritis and viral, bacterial, fungal, helminthic and
CC   protozoal infections). The sequence presented is the human KLIMP protein
XX
SQ   Sequence 1103 AA;

  Query Match           60.9%;  Score 1117;  DB 6;  Length 1103;
  Best Local Similarity  61.6%;  Pred. No. 1.3e-100;
  Matches  220;  Conservative   59;  Mismatches   62;  Indels   16;  Gaps    5;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| ||||||||||  : |||:| |:|| | :  |           |   | ||:|
Db          3 GASVKVAVRVRPFNARETSQDAKCVVSMQGNTTSIINP----------KQSKDAPKSFT 51

Qy         64 FDRSYWSFDKNA-PNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122
              || ||||      | :| |: :::|:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWSHTSTEDPQFASQQQVYRDIGEEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGRQ 111

Qy        123 K--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
              :  : |::|::|:|:| |::| |    |: :|||||:||| |||||||| ::|:|:|||
Db        112 EPGQQGIVPQLCEDLFSRVSENQ-SAQLSYSVEVSYMEIYCERVRDLLNPKSRGSLRVRE 170

Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240
              ||  ||||:||:|| | |: :| :||| |||||||||||||||||||||:  ||: |
Db        171 HPILGPYVQDLSKLAVTSYADIADLMDCGNKARTVAATNMNETSSRSHAVFTIVFTQRCH 230

Qy        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS 300
              |: | :|:|||:|||||||||||||| |:|| |  ||||| ||:||:|||:||:||||| |
Db        231 DQLTGLDSEKVSKISLVDLAGSERADSSGARGMGLKEGANINKSLTTLGKVISALADMQS 290

Qy        301 GKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK 357
               |::|:  :|||||||||||::||||| ||||||:||||||:||||||||||  |
Db        291 -KKRKSDFIPYRDSVLTWLLKENLGGNSRTAMIAALSPADINYEETLSTLRYADRTK 346


RESULT 18
ADG63388
ID   ADG63388 standard; protein; 1103 AA.
XX
AC   ADG63388;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human kinesin-like motor protein, KLIMP.
XX
KW   Human; kinesin-like motor protein; KLIMP; cancer; neurological disorder;
KW   Alzheimer's disease; Parkinson's disease;
KW   disorder of vesicular transport; cystic fibrosis; hypercholesterolaemia;
KW   diabetes; Grave's disease; Addison's disease; AIDS;
KW   autoimmune haemolytic anaemia; glomerulonephritis;
KW   inflammatory bowel disease; rheumatoid arthritis;
KW   systemic lupus erythematosus; infections; INCYTE 1281811.
XX
OS   Homo sapiens.
XX
PN   US2003207318-A1.
XX
PD   06-NOV-2003.
XX
PF   09-JUN-2003; 2003US-00458162.
XX
PR   28-SEP-1998;   98US-00162373.
PR   21-DEC-1999;   99US-00467946.
PR   02-MAY-2001; 2001US-00847874.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Tang YT,  Corley NC,  Guegler KJ,  Patterson C;
XX
DR   WPI; 2003-901054/82.
DR   N-PSDB; ADG63389.
XX
PT   New human kinesin-like motor protein and polynucleotides, useful for
PT   diagnosing, preventing or treating diseases or conditions associated with
PT   aberrant protein expression, e.g. cancer, neurological disorders, AIDS or
PT   diabetes.
XX
PS   Claim 1; SEQ ID NO 1; 40pp; English.
XX
CC   The invention relates to a new isolated polypeptide comprising the human
CC   kinesin-like motor protein (KLIMP) appearing as ADG63388, a naturally-
CC   occurring amino acid sequence that is at least 90% identical to KLIMP or
CC   a biologically active or immunogenic fragment of KLIMP. Also included are
```

CC an isolated polynucleotide (NA) encoding KLIMP (appearing as ADG63389, a
CC recombinant polynucleotide comprising a promoter sequence operably linked
CC to the KLIMP NA, a cell transformed with the recombinant polynucleotide,
CC a transgenic organism comprising the recombinant polynucleotide, methods
CC of producing or purifying KLIMP, an isolated antibody, which specifically
CC binds to KLIMP, methods of detecting a target polynucleotide or KLIMP in
CC a sample, compositions comprising the polypeptide, an agonist compound,
CC an antagonist compound or an antibody, and an excipient, methods of
CC treating diseases or conditions associated with decreased expression or
CC overexpression of KLIMP, methods of screening for a compound that is
CC effective as an agonist or antagonist of KLIMP (that specifically binds
CC to KLIMP, that modulates the activity of KLIMP, or is effective in
CC altering expression of the target polynucleotide), a method of screening
CC for potential toxicity of a test compound, a diagnostic test for a
CC condition or disease associated with the expression of KLIMP in a
CC biological sample, methods of diagnosing a condition or disease
CC associated with the expression of KLIMP in a subject, a method of
CC generating an expression profile of a sample containing the
CC polynucleotides and an array comprising different nucleotide molecules
CC affixed at distinct physical locations on a solid substrate, where at
CC least one nucleotide molecule comprises a first oligonucleotide or
CC polynucleotide sequence specifically hybridisable with at least 30
CC contiguous nucleotides of the target polynucleotide. The polypeptides and
CC polynucleotides are useful in diagnosing, preventing or treating diseases
CC or conditions associated with the decreased expression or overexpression
CC of KLIMP, such as cancer, neurological disorders (e.g. Alzheimer's
CC disease or Parkinson's disease), disorders of vesicular transport (e.g.
CC cystic fibrosis, hypercholesterolaemia, diabetes, Grave's disease or
CC Addison's disease), AIDS, autoimmune haemolytic anaemia,
CC glomerulonephritis, inflammatory bowel disease, rheumatoid arthritis,
CC systemic lupus erythematosus, or infections (e.g. viral, bacterial,
CC fungal, helminthic or protozoal). These are also useful in assessing the
CC effects of exogenous compounds on the expression of nucleic acid and
CC amino acid sequences of KLIMP. The KLIMP or its fragments are useful in
CC screening compounds for effectiveness as agonist or antagonist of the
CC polypeptides, or in altering the expression of the target polynucleotide
CC and compounds that specifically bind to or modulate the activity of the
CC polypeptide. The microarray is useful in monitoring or measuring protein-
CC protein interactions, drug-target interactions, and gene expression
CC profiles. The present sequence represents human KLIMP (INCYTE 1281811).
XX
SQ Sequence 1103 AA;

Query Match 60.9%; Score 1117; DB 7; Length 1103;
Best Local Similarity 61.6%; Pred. No. 1.3e-100;
Matches 220; Conservative 59; Mismatches 62; Indels 16; Gaps 5;

```
Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| ||||||||||  : |||:| |:|| | :  |           |   | ||:|
Db          3 GASVKVAVRVRPFNARETSQDAKCVVSMQGNTTSIINP----------KQSKDAPKSFT 51

Qy         64 FDRSYWSFDKNA-PNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122
              || ||||      | :| |: :::|:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWSHTSTEDPQFASQQQVYRDIGEEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGRQ 111

Qy        123 K--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
              :  : |::|::|:|:| |::| |    |: :|||||:||| |||||||| ::|:|:|||
Db        112 EPGQQGIVPQLCEDLFSRVSENQ-SAQLSYSVEVSYMEIYCERVRDLLNPKSRGSLRVRE 170

Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240
              ||  ||||:||:|| | |: :| :||| |||||||||||||||||||||:  ||: |
Db        171 HPILGPYVQDLSKLAVTSYADIADLMDCGNKARTVAATNMNETSSRSHAVFTIVFTQRCH 230

Qy        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS 300
              |: | :|:|||:|||||||||||||| |:|| |  ||||| ||:||:|||:||:||||| |
Db        231 DQLTGLDSEKVSKISLVDLAGSERADSSGARGMGLKEGANINKSLTTLGKVISALADMQS 290

Qy        301 GKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK 357
               |::|:  :|||||||||||::|||||  ||||||:||||||:||||||||||  |
Db        291 -KKRKSDFIPYRDSVLTWLLKENLGGNSRTAMIAALSPADINYEETLSTLRYADRTK 346
```

RESULT 19

AAE35317
ID AAE35317 standard; protein; 1770 AA.
XX
AC AAE35317;
XX
DT 17-JUN-2003 (first entry)
XX
DE Mouse KIF1Bbeta protein.
XX
KW KIF1Bb protein; gene therapy; molecular motor protein; kinesin; mouse;
KW kifB1beta gene-associated disease; Charcot-Marie-Tooth disease type 2A;
KW muscular; transgenic.
XX
OS Mus musculus.
XX
PN WO200297079-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-JP005226.
XX
PR 29-MAY-2001; 2001US-0293513P.
XX
PA (UYTY) UNIV TOKYO.
XX
PI Hirokawa N, Hayashi Y;
XX
DR WPI; 2003-167270/16.
DR N-PSDB; AAD53964.
XX
PT New KIF1Bb polypeptide having motor activity that transports synaptic
PT vesicle precursor, is useful for developing therapeutic or preventive
PT agent for kif1Bb gene-associated diseases e.g. Charcot-Marie-Tooth
PT disease type 2A.
XX
PS Claim 1; Page 72-78; 44pp; English.
XX
CC The invention relates to KIF1Bb protein which belongs to kinesin
CC superfamily of molecular motor proteins (KIFs). KIF1Bb is useful for
CC screening for a compound binding to it. Composition comprising the
CC selected compound is useful for treating, alleviating, or preventing a
CC kifB1beta gene-associated disease, in particular Charcot-Marie-Tooth
CC disease type 2A. Transgenic non-human vertebrate, are useful for
CC screening for a candidate compound for treating, alleviating, or
CC preventing a kif1Bbeta gene-associated disease. KIF1Bb DNA is useful for
CC gene therapy and for recombinant production of polypeptides. KIF1Bb
CC antibody is useful for affinity purification of KIF1Bb and for detecting
CC expression of kif1Bbeta gene at the protein level. The present sequence
CC is mouse KIF1Bbeta protein
XX
SQ Sequence 1770 AA;

Query Match 60.7%; Score 1114; DB 6; Length 1770;
Best Local Similarity 61.3%; Pred. No. 5.4e-100;
Matches 219; Conservative 59; Mismatches 63; Indels 16; Gaps 5;

```
Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||  : :|||::|:|| | :  |   :|            ||:|:
Db          3 GASVKVAVRVRPFNSRETSKESKCIIQMQGNSTSIINPKNPKE----------APKSFS 51

Qy         64 FDRSYWSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122
              || ||||      | :| |  :: |:|  :| :||:||| |||||||||:||||:|||
Db         52 FDYSYWSHTSPEDPCFASQNRVYNDIGKEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGKQ 111

Qy        123 KEH--GVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
              :|   |:||::|:::| :||:   :: :: :|||||:||| |||||||||  ||||:|||
Db        112 EESQAGIIPQLCEELFEKIND-NCNEEMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE 170

Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240
              ||  |||||||:|| | |: :| :||| |||||||||||||||||||||:  |||
Db        171 HPLLGPYVEDLSKLAVTSYTDIADLMDAGNKARTVAATNMNETSSRSHAVFTIVFTQKKQ 230

Qy        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS 300
```

```
           | || : ||||:||||||||||||| |||| | |||||| ||:||:|||:||:|||::|
Db        231 DPETNLSTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEVSK 290

Qy        301 GKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK 357
              |:||   :||||||||||:::||||| |||:||:||||||::|||||||| ||
Db        291 -KKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADRAK 346


RESULT 20
ADJ95088
ID   ADJ95088 standard; protein; 1805 AA.
XX
AC   ADJ95088;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Novel NOVX protein sequence #158.
XX
KW   antidiabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic;
KW   anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic;
KW   neuroprotective; antiparkinsonian; anticonvulsant; osteopathic;
KW   antiarthritic; antiinflammatory; dermatological; antiasthmatica;
KW   antilipemic; gene therapy; metabolic disorder; diabetes; obesity;
KW   infectious disease; anorexia; cancer; cardiovascular disease;
KW   hypertension; atherosclerosis; neurodegenerative disorder;
KW   Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;
KW   osteoarthritis; hematopoietic disorder; inflammatory skin disorder;
KW   asthma; dyslipidemia; neurogenesis; cell differentiation;
KW   cell proliferation; hematopoiesis; wound healing; angiogenesis;
KW   chromosome mapping; tissue typing; pharmacogenomic.
XX
OS   Homo sapiens.
XX
PN   WO2003040325-A2.
XX
PD   15-MAY-2003.
XX
PF   05-NOV-2002; 2002WO-US035464.
XX
PR   05-NOV-2001; 2001US-0338626P.
PR   06-NOV-2001; 2001US-0333072P.
PR   09-NOV-2001; 2001US-0348283P.
PR   15-NOV-2001; 2001US-0335610P.
PR   16-NOV-2001; 2001US-0338543P.
PR   20-NOV-2001; 2001US-0331630P.
PR   20-NOV-2001; 2001US-0331641P.
PR   21-NOV-2001; 2001US-0332152P.
PR   27-NOV-2001; 2001US-0333461P.
PR   28-NOV-2001; 2001US-0333912P.
PR   28-NOV-2001; 2001US-0334027P.
PR   29-NOV-2001; 2001US-0334300P.
PR   30-NOV-2001; 2001US-0334421P.
PR   30-NOV-2001; 2001US-0334526P.
PR   04-DEC-2001; 2001US-0336576P.
PR   04-DEC-2001; 2001US-0336664P.
PR   07-DEC-2001; 2001US-0338314P.
PR   07-DEC-2001; 2001US-0338390P.
PR   10-DEC-2001; 2001US-0339006P.
PR   10-DEC-2001; 2001US-0339008P.
PR   11-DEC-2001; 2001US-0339286P.
PR   01-FEB-2002; 2002US-0353280P.
PR   01-FEB-2002; 2002US-0353288P.
PR   04-FEB-2002; 2002US-0354392P.
PR   04-FEB-2002; 2002US-0354393P.
PR   04-FEB-2002; 2002US-0354409P.
PR   27-FEB-2002; 2002US-0359944P.
PR   27-FEB-2002; 2002US-0360148P.
PR   05-MAR-2002; 2002US-0361790P.
PR   05-MAR-2002; 2002US-0361833P.
PR   05-MAR-2002; 2002US-0361925P.
PR   05-MAR-2002; 2002US-0362230P.
PR   05-MAR-2002; 2002US-0362625P.
PR   13-MAR-2002; 2002US-0364000P.
PR   13-MAR-2002; 2002US-0364181P.
PR   13-MAR-2002; 2002US-0364182P.
PR   13-MAR-2002; 2002US-0364197P.
PR   13-MAR-2002; 2002US-0364227P.
PR   17-MAY-2002; 2002US-0381621P.
PR   28-MAY-2002; 2002US-0383675P.
PR   17-JUL-2002; 2002US-0396703P.
PR   06-AUG-2002; 2002US-0401552P.
PR   07-AUG-2002; 2002US-0401594P.
PR   07-AUG-2002; 2002US-0401787P.
PR   15-AUG-2002; 2002US-0403619P.
PR   20-AUG-2002; 2002US-0404821P.
PR   23-AUG-2002; 2002US-0405368P.
PR   23-AUG-2002; 2002US-0405402P.
PR   23-AUG-2002; 2002US-0405496P.
PR   23-AUG-2002; 2002US-0405631P.
PR   26-AUG-2002; 2002US-0406125P.
PR   04-NOV-2002; 2002US-00287226.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Agee ML,  Alsobrook JP,  Berghs C,  Boldog FL,  Burgess CE,  Chant JS;
PI   Chaudhuri A,  Dipippo VA,  Edinger SR,  Eisen A,  Ellerman K;
PI   Gangolli EA,  Gorman L,  Gerlach VL,  Ji W,  Kekuda R,  Khramtsov NV;
PI   Li L,  Malyankar UM,  Macdougall JR,  Mezes PS,  Miller CE,  Millet I;
PI   Ooi CE,  Ort T,  Padigaru M,  Patturajan M,  Rastelli L,  Rieger DK;
PI   Rothenberg ME,  Shenoy SG,  Spaderna SK,  Spytek KA,  Taupier RJ;
PI   Vernet CAM,  Zerhusen BD,  Zhong M;
XX
DR   WPI; 2003-441551/41.
DR   N-PSDB; ADJ95087.
XX
PT   New isolated NOVX polypeptides and polynucleotides, useful for
PT   preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT   osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT   asthma, or infections.
XX
PS   Claim 1; SEQ ID NO 316; 800pp; English.
XX
CC   The invention relates to novel isolated polypeptides, mature forms of
CC   these, or a sequence that is at least 95 % identical to, or having one or
CC   more conservative amino acid substitutions in the polypeptides. The
CC   polypeptides, nucleic acid molecules and antibodies are useful in the
CC   manufacture of a medicament for treating a syndrome associated with a
CC   human disease, preferably a NOVX-associated disorder. The nucleic acid
CC   molecules, polypeptides and antibodies are useful for treating,
CC   preventing or diagnosing diseases such metabolic disorders, diabetes,
CC   obesity, infectious diseases (viral, bacterial, fungal, helminthic, and
CC   protozoal), anorexia, cancer, cardiovascular diseases (hypertension,
CC   atherosclerosis), neurodegenerative disorders, Alzheimer's disease,
CC   Parkinson's disease, epilepsy, immune disorders (osteoarthritis),
CC   hematopoietic disorders, inflammatory skin disorders, asthma, and various
CC   dyslipidemias. The nucleic acids and polypeptides may also be used as
CC   targets for the identification of small molecules that modulate or
CC   inhibit e.g. neurogenesis, cell differentiation, cell proliferation,
CC   hematopoiesis, wound healing and angiogenesis, in gene therapy, in
CC   generation of antibodies that bind immunospecifically to NOVX substances
CC   for use in therapeutic or diagnostic methods. The nucleic acids are
CC   further used as hybridization probes, in chromosome mapping, tissue
CC   typing, preventive medicine, and pharmacogenomics. This sequence
CC   corresponds to one of the NOVX polypeptides of the invention.
XX
SQ   Sequence 1805 AA;

  Query Match             60.7%;  Score 1112.5;  DB 7;  Length 1805;
  Best Local Similarity   61.5%;  Pred. No. 7.9e-100;
  Matches  220;  Conservative   59;  Mismatches   62;  Indels   17;  Gaps    6;

Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
              | ::|| |||||||:||  : :|||::|:|| | :  |  :|           ||:|:
Db          3 GASVKVAVRVRPFNSRETSKESKCIIQMQGNSTSIINPKNPKE----------APKSFS 51

Qy         64 FDRSYWSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122
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Db         52 FDYSYWSHTSPEDPCFASQNRVYNDIGKEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGKQ 111

Qy        123 KEH--GVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180

Db        112 EESQAGIIPQLCEELFEKIND-NCNEEMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE 170

Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240

Db        171 HPLLGPYVEDLSKLAVTSYTDIADLMDAGNKARTVAATNMNETSSRSHAVFTIVFTQKKH 230

Qy        241 DEETKMDTEK-VAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMS 299

Db        231 DNETNLSTEKVVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEVS 290

Qy        300 SGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK 357

Db        291 K-KKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADRAK 347
```

RESULT 21
ADV50414
ID ADV50414 standard; protein; 365 AA.
XX
AC ADV50414;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human KIF1B motor domain.
XX
KW ATPase modulator; kinesin family 1B; KIF1B; kinesin; cell proliferation;
KW hyperproliferative disorders; cancer; breast tumor; restenosis;
KW cardiovascular disease; autoimmune disease; immune disorder; arthritis;
KW inflammation; musculoskeletal disease; graft rejection;
KW inflammatory bowel disease; gastrointestinal disease; cytostatic;
KW vasotropic; immunosuppressive; antiarthritic; antiinflammatory;
KW gastrointestinal-gen. .
XX
OS Homo sapiens.
XX
PN WO2004109290-A2.
XX
PD 16-DEC-2004.
XX
PF 28-MAY-2004; 2004WO-US017234.
XX
PR 30-MAY-2003; 2003US-0474488P.
PR 03-JUN-2003; 2003US-0475873P.
PR 17-MAR-2004; 2004US-0553838P.
XX
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (MERI) MERCK & CO INC.
XX
PI Mao M, Linsley PS, Buser CA, Marshall CG, Kim AS;
XX
DR WPI; 2005-057663/06.
XX
PT Screening for modulators of target protein e.g., kinesin family 14
PT protein, by contacting target protein with candidate agent, and
PT determining whether candidate agent modulates activity of target protein.
XX
PS Example 7; SEQ ID NO 21; 118pp; English.
XX
CC The invention relates to a method (M1) of screening for modulators of a
CC target protein. The method involves contacting the target protein with
CC candidate agent, and determining whether the candidate agent modulates
CC activity of target protein, where the target protein comprises a sequence
CC that has more than 80% amino acid sequence identity to a fully defined
CC kinesin family 14 (KIF14) protein (SEQ ID No:2) or the KIF14 motor domain
CC sequence (SEQ ID No:3). Also described are: a method (M2) for modulating
CC cell proliferation, a method (M3) for treating a subject with a cellular
CC hyperproliferation disorder, a method (M4) for identifying candidate
CC subjects for treatment with an inhibitor of the activity of a target
CC protein, and a kit for screening for modulators of a target protein. A
CC cell viability assay, cell morphology assay, cell proliferation assay,
CC cell cycle distribution assay or apoptosis assay is used for determining
CC whether the candidate agent modulates the activity of the target protein.
CC The target protein comprises SEQ ID No:2, SEQ ID No:3, or a fragment of
CC SEQ ID No:3 having ATPase activity. The modulator is an inhibitor such as
CC RNA inhibitor, which is a KIF14 RNA inhibitor. The KIF14 RNA inhibitor
CC comprises sequences such as those disclosed in SEQ ID Nos 8, 9 or 23.
CC Method (M1) is useful for screening for modulators of a target protein,
CC particularly for screening modulators of KIF14 or KIF14 motor domain.
CC Method (M2) is useful for treating a subject with a cellular
CC hyperproliferation disorder such as cancer, preferably breast cancer.
CC Method (M3) is useful for treating restenosis, autoimmune disease,
CC arthritis, graft rejection or inflammatory bowel disease. This sequence
CC represents human KIF1B motor domain.
XX
SQ Sequence 365 AA;

Query Match 60.6%; Score 1111; DB 9; Length 365;
Best Local Similarity 60.7%; Pred. No. 8.2e-101;
Matches 218; Conservative 59; Mismatches 62; Indels 20; Gaps 5;

```
Qy          4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63

Db          3 GASVKVAVRVRPFNSRETSKESKCIIQMQGNSTSIINPKNPKE----------APKSFS 51

Qy         64 FDRSYWSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122

Db         52 FDYSYWSHTSPEDPCFASQNRVYNDIGKEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGKQ 111

Qy        123 KEH--GVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180

Db        112 EESQAGIIPQLCEELFEKIND-NCNEEMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE 170

Qy        181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240

Db        171 HPLLGPYVEDLSKLAVTSYTDIADLMDAGNKARTVAATNMNETSSRSHAVFTIVFTQKKH 230

Qy        241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM-- 298

Db        231 DNETNLSTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEVDN 290

Qy        299 ---SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYAD 354

Db        291 CTSKSKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYAD 349
```

RESULT 22
ABB63908
ID ABB63908 standard; protein; 1773 AA.
XX
AC ABB63908;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 18516.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX

```
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   N-PSDB; ABL08011.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signaling and cell-cell
PT   interactions.
XX
PS   Disclosure; SEQ ID NO 18516; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC   ABB72072). The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1773 AA;

  Query Match             60.3%;  Score 1106.5;  DB 4;  Length 1773;
  Best Local Similarity   62.4%;  Pred. No. 3e-99;
  Matches  222;  Conservative   52;  Mismatches   69;  Indels   13;  Gaps    4;

Qy          6 NIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFAFD 65
              ::|| |||||||:||| | :|||: | |  | :| |        |       |  | | ||
Db         32 SVKVAVRVRPFNSREIARESKCIIEMAGATTAITNP--------KVPPNTSDSVKRFNFD 83

Qy         66 RSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYGKE- 124
                |||| | :  ::: |  :::|:|  :| ::| ||| |||||||||:||||:|||  :|
Db         84 YSYWSHDHHDADFSTQSMVYKDIGEEMLQHSFDGYNVCIFAYGQTGAGKSYTMMGRQEEQ 143

Qy        125 -HGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVREHPS 183
               |:|| ||:|:| || : : | :|  :|||||:||| |||||||||  ||||:|||||
Db        144 QEGIIPMICKDLFTRIQDTETD-DLKYSVEVSYMEIYCERVRDLLNPKNKGNLRVREHPL 202

Qy        184 TGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWHDEE 243
              |||||||:|| |  :|:| :|:|||||||||||||||||||||||||:  ||: ||
Db        203 LGPYVEDLSKLAVTDYQDIHDLIDEGNKARTVAATNMNETSSRSHAVFTIFFTQRRHDLM 262

Qy        244 TKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSSGKQ 303
              | : ||||:|||||||||||||| |||| | |||||| ||:||:|||:||:|||:::| |:
Db        263 TNLTTEKVSKISLSVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEVASKKK 322

Qy        304 --KKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK 357
                ||   :||||| |||||:::|||||  ||||||||||||::||||||||| ||
Db        323 NTKKADFIPYRDSALTWLLRENLGGNSKTAMIAAISPADINYDETLSTLRYADRAK 378


RESULT 23
AAU74840
ID   AAU74840 standard; protein; 1362 AA.
XX
AC   AAU74840;
XX
DT   10-APR-2002  (first entry)
XX
DE   Human HsKif13a protein sequence.
XX
KW   HsKif13a; human; kinesin; microtubule motor protein; cytostatic;
KW   vulnerary; antirheumatic; antiarthritic; antigout; antiinflammatory;
KW   vasotropic; neuroprotective; cytoskeletal; atherosclerosis; cancer;
KW   haematopoietic tumour; tumour metastasis; benign tumour; haemangioma;
KW   acoustic neuroma; wound healing; rheumatoid arthritis; psoriasis;
KW   Behcet's disease; gout; gouty arthritis; angiogenesis;
KW   rheumatoid arthritis; diabetic retinopathy; neurological disorder;
KW   vesicular transport disorder.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          1. .352
FT                   /note= "HsKif13a motor domain, this sequence is
FT                   specifically claimed in claim 8 of the specification"
FT   Misc-difference 540
FT                   /label= Unknown
FT                   /note= "Encoded by AGN"
FT   Misc-difference 541. .563
FT                   /label= Xaa
FT                   /note= "Amino acid residues 541-563 are all Xaa, and are
FT                   all encoded by NNN"
FT   Misc-difference 564
FT                   /label= Unknown
FT                   /note= "Encoded by NNA"
FT   Misc-difference 747. .769
FT                   /note= "Amino acid residues 747-769 are all Xaa, and are
FT                   all encoded by NNN"
FT   Misc-difference 770
FT                   /label= Unlnown
FT                   /note= "Encoded by NGT"
XX
PN   WO200192467-A2.
XX
PD   06-DEC-2001.
XX
PF   26-MAY-2001; 2001WO-US017148.
XX
PR   26-MAY-2000; 2000US-00580828.
XX
PA   (CYTO-) CYTOKINETICS INC.
XX
PI   Beraud C,  Freedman R;
XX
DR   WPI; 2002-075464/10.
DR   N-PSDB; ABK13131.
XX
PT   Human microtubule motor protein, HsKif13a, useful for screening
PT   modulators of HsKif13a which are used for modulating cytoskeletal system
PT   in conditions of benign tumors and rheumatoid arthritis.
XX
PS   Claim 11; Fig 2; 55pp; English.
XX
CC   This invention relates to the nucleic acid and protein sequence of a
CC   novel microtubule motor protein HsKif13a. The protein of the invention
CC   may have cytostatic; vulnerary; antirheumatic; antiarthritic; antigout;
CC   antiinflammatory; vasotropic; neuroprotective activities and may act as a
CC   cytoskeletal system modulator. The HsKif13a nucleic acid is useful for
CC   screening for modulators of HsKif13a, such modulators would be useful for
CC   modulating cytoskeletal system for treating conditions such as abnormal
CC   stimulation of endothelial cells (e.g., atherosclerosis), solid and
CC   haematopoietic tumours and tumour metastasis, benign tumours, e.g.,
CC   haemangiomas, acoustic neuromas, etc., abnormal wound healing, rheumatoid
CC   arthritis, Behcet's disease, gout or gouty arthritis, abnormal
CC   angiogenesis accompanying: rheumatoid arthritis, psoriasis, diabetic
CC   retinopathy, etc. The sequences of the invention are useful for the
CC   diagnosis, treatment, or prevention of cancer, neurological and vesicular
CC   transport disorders. Nucleic acids encoding the kinesins are useful for
CC   identifying polymorphic variants, orthologues, alleles and homologues of
CC   HsKif13a. HsKif13a and its homologues are also useful as diagnostic tools
CC   in vitro. The kinesins and in particular their motor domains can be used
CC   for separation of a specific ligand from a heterologous mixture in
CC   aqueous solution. The kinesins and in particular their motor domains can
CC   also be used in the field of nanotechnology. The present sequence
CC   represents the human HsKif13a protein sequence of the invention
XX
SQ   Sequence 1362 AA;

  Query Match             58.0%;  Score 1063;  DB 5;  Length 1362;
  Best Local Similarity   60.1%;  Pred. No. 4e-95;
  Matches  212;  Conservative   62;  Mismatches   69;  Indels   10;  Gaps    5;

Qy          7 IKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFAFDR 66
```

```
                :|| ||||| | ||::   ||:| ||||||:| |||   ::  :        || ||||
Db          6 VKVAVRVRPMNRRELELNTKCVVEMEGNQTVLHPPPSNTKQGERK------PPKVFAFDY 59

Qy         67 SYWSFDK-NAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYGKEH 125
               :|| |: |   || || :|: ||  :|: ||:||| ||||||||||||:||||: ::
Db         60 CFWSMDESNTTKYAGQEVVFKCLGEGILEKAFQGYNACIFAYGQTGSGKSFSMMGHAEQL 119

Qy        126 GVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNP-STKGNLKVREHPST 184
               |:|||:|  :|:||: |:::::  |  |||||:|||||:|||||:|  :: :||||||
Db        120 GLIPRLCCALFKRIS-LEQNESQTFKVEVSYMEIYNEKVRDLLDPKGSRQSLKVREHKVL 178

Qy        185 GPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWHDEET 244
               ||||: |::| | ||::||::|| ||||:|||||||||| |||||||| : :||  :| ::
Db        179 GPYVDGLSQLAVTSFEDIESLMSEGNKSRTVAATNMNEESSRSHAVFNIIITQTLYDLQS 238

Qy        245 KMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSSGKQK 304
                   |||:|:|||||||||| : ||| | |||||: ||:||:||| ||::||| ::||
Db        239 GNSGEKVSKVSLVDLAGSERVSKTGAAGERLKEGSNINKSLTTLGLVISSLADQAAGK-G 297

Qy        305 KNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK 357
               |:: ||||||||||||||:||||| |:||| |||| |:||||||||||| ||
Db        298 KSKFVPYRDSVLTWLLKDNLGGNSQTSMIATISPAADNYEETLSTLRYADRAK 350
```

RESULT 24
ABP68930
ID ABP68930 standard; protein; 1805 AA.
XX
AC ABP68930;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human polypeptide SEQ ID NO 977.
XX
KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic.
XX
OS Homo sapiens.
XX
PN WO200270539-A2.
XX
PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-US005095.
XX
PR 05-MAR-2001; 2001US-00799451.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX
DR WPI; 2002-759812/82.
DR N-PSDB; ABZ11147.
XX
PT New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.
XX
PS Claim 9; SEQ ID NO 977; 1012pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising a
CC nucleotide sequence selected from any of 948 sequences (ABZ11119-
CC ABZ12066) or their mature protein coding portion, active domain coding
CC protein or complementary sequences. The polynucleotides are useful for
CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical
CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1805 AA;

```
  Query Match             58.0%;  Score 1063;  DB 5;  Length 1805;
  Best Local Similarity   60.1%;  Pred. No. 6.4e-95;
  Matches  212;  Conservative   62;  Mismatches   69;  Indels   10;  Gaps    5;

Qy          7 IKVVVRVRPFNARELDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFAFDR 66
               :|| ||||| | ||::   ||:| ||||||:| |||   ::  :        || ||||
Db          6 VKVAVRVRPMNRRELELNTKCVVEMEGNQTVLHPPPSNTKQGERK------PPKVFAFDY 59

Qy         67 SYWSFDK-NAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYGKEH 125
               :|| |: |   || || :|: ||  :|: ||:||| ||||||||||||:||||: ::
Db         60 CFWSMDESNTTKYAGQEVVFKCLGEGILEKAFQGYNACIFAYGQTGSGKSFSMMGHAEQL 119

Qy        126 GVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNP-STKGNLKVREHPST 184
               |:|||:|  :|:||: |:::::  |  |||||:|||||:|||||:|  :: :||||||
Db        120 GLIPRLCCALFKRIS-LEQNESQTFKVEVSYMEIYNEKVRDLLDPKGSRQSLKVREHKVL 178

Qy        185 GPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWHDEET 244
               ||||: |::| | ||::||::|| ||||:|||||||||| |||||||| : :||  :| ::
Db        179 GPYVDGLSQLAVTSFEDIESLMSEGNKSRTVAATNMNEESSRSHAVFNIIITQTLYDLQS 238

Qy        245 KMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSSGKQK 304
                   |||:|:|||||||||| : ||| | |||||: ||:||:||| ||::||| ::||
Db        239 GNSGEKVSKVSLVDLAGSERVSKTGAAGERLKEGSNINKSLTTLGLVISSLADQAAGK-G 297

Qy        305 KNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK 357
               |:: ||||||||||||||:||||| |:||| |||| |:||||||||||| ||
Db        298 KSKFVPYRDSVLTWLLKDNLGGNSQTSMIATISPAADNYEETLSTLRYADRAK 350
```

RESULT 25
ABB62962
ID ABB62962 standard; protein; 1921 AA.
XX
AC ABB62962;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 15678.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.

```
DR   N-PSDB; ABL07065.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signaling and cell-cell
PT   interactions.
XX
PS   Disclosure; SEQ ID NO 15678; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC   ABB72072). The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1921 AA;

  Query Match             56.1%;  Score 1028;  DB 4;  Length 1921;
  Best Local Similarity   60.3%;  Pred. No. 2.1e-91;
  Matches  213;  Conservative   45;  Mismatches   85;  Indels   10;  Gaps    4;

Qy          7 IKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFAFDR 66
              ||| ||||||| |||:   |||| ||  |||| ||  |:  ||        || ||||
Db          6 IKVAVRVRPFNRREIELDTKCIVEMEKQQTILQNPPPLEKIERKQ-------PKTFAFDH 58

Qy         67 SYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYGKEHG 126
               ::| :    |:| || :|  :|  :|||||:||| ||||||||||||:||  :  |
Db         59 CFYSLNPEDENFASQETVFDCVGRGILDNAFQGYNACIFAYGQTGSGKSYTMMGTQESKG 118

Qy        127 VIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPS-TKGNLKVREHPSTG 185
              :|||:|  :|  |   :    |   |||||:|||||:| |||:|   | :||||||   |
Db        119 IIPRLCDQLFSAIAN-KSTPELMYKVEVSYMEIYNEKVHDLLDPKPNKQSLKVREHNVMG 177

Qy        186 PYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWHDEETK 245
              |||: |::| | |:|:|:||| ||||:||||||||  ||||||||:: |||   |: |
Db        178 PYVDGLSQLAVTSYQDIDNLMTEGNKSRTVAATNMNAESSRSHAVFSVVLTQILTDQATG 237

Qy        246 MDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSSGKQKK 305
              :  |||:::|||||||||||  ||| | |||||: ||:||:||| ||: ||| |:||:
Db        238 VSGEKVSRMSLVDLAGSERAVKTGAVGDRLKEGSNINKSLTTLGLVISKLADQSNGKKSG 297

Qy        306 N-QLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK 357
              | : |||||||||||||:||||| | |:| |||:  |:||||||||||| ||
Db        298 NDKFVPYRDSVLTWLLKDNLGGNSRTVMVATISPSADNYEETLSTLRYADRAK 350


RESULT 26
AAU19569
ID   AAU19569 standard; protein; 757 AA.
XX
AC   AAU19569;
XX
DT   04-DEC-2001  (first entry)
XX
DE   Human diagnostic and therapeutic polypeptide (DITHP) #155.
XX
KW   Human; receptor; diagnostic; therapeutic; gene therapy; vaccine;
KW   cell proliferative disorder; Crohn's disease; lymphoma; leukaemia;
KW   acquired immune deficiency syndrome; AIDS; autoimmune disorder;
KW   respiratory disorder.
XX
OS   Homo sapiens.
XX
PN   WO200162927-A2.
XX
PD   30-AUG-2001.
XX
PF   21-FEB-2001; 2001WO-US006059.
XX
PR   24-FEB-2000; 2000US-0184693P.
PR   24-FEB-2000; 2000US-0184697P.
PR   24-FEB-2000; 2000US-0184698P.
PR   24-FEB-2000; 2000US-0184768P.
PR   24-FEB-2000; 2000US-0184769P.
PR   24-FEB-2000; 2000US-0184770P.
PR   24-FEB-2000; 2000US-0184771P.
PR   24-FEB-2000; 2000US-0184772P.
PR   24-FEB-2000; 2000US-0184773P.
PR   24-FEB-2000; 2000US-0184774P.
PR   24-FEB-2000; 2000US-0184776P.
PR   24-FEB-2000; 2000US-0184777P.
PR   24-FEB-2000; 2000US-0184797P.
PR   24-FEB-2000; 2000US-0184813P.
PR   24-FEB-2000; 2000US-0184837P.
PR   24-FEB-2000; 2000US-0184841P.
PR   24-FEB-2000; 2000US-0185213P.
PR   24-FEB-2000; 2000US-0185216P.
PR   12-MAY-2000; 2000US-0203785P.
PR   15-MAY-2000; 2000US-0204226P.
PR   16-MAY-2000; 2000US-0204525P.
PR   16-MAY-2000; 2000US-0204821P.
PR   16-MAY-2000; 2000US-0204908P.
PR   16-MAY-2000; 2000US-0205232P.
PR   17-MAY-2000; 2000US-0204815P.
PR   17-MAY-2000; 2000US-0204863P.
PR   17-MAY-2000; 2000US-0205221P.
PR   17-MAY-2000; 2000US-0205285P.
PR   17-MAY-2000; 2000US-0205286P.
PR   17-MAY-2000; 2000US-0205287P.
PR   17-MAY-2000; 2000US-0205323P.
PR   17-MAY-2000; 2000US-0205324P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Panzer SR,  Spiro PA,  Banville SC,  Shah P,  Chalup MS,  Chang SC;
PI   Chen A,  D'sa SA,  Amshey S,  Dahl CR,  Dam TC,  Daniels SE,  Dufour GE;
PI   Flores V,  Fong WT,  Greenawalt LB,  Hillman JL,  Jones AL,  Liu TF;
PI   Roseberry AM,  Rosen BH,  Russo FD,  Stockdreher TK,  Daffo A;
PI   Wright RJ,  Yap PE,  Yu JY,  Bradley DL,  Bratcher SR,  Chen W;
PI   Cohen HJ,  Hodgson DM,  Lincoln SE,  Jackson S;
XX
DR   WPI; 2001-502867/55.
DR   N-PSDB; AAS31140.
XX
PT   Polynucleotides encoding diagnostic and therapeutic proteins, e.g.
PT   enzymes, hormones and receptors, useful in diagnostics and therapeutics.
XX
PS   Claim 27; Page 488-490; 522pp; English.
XX
CC   The invention relates to polynucleotides (I) encoding diagnostic and
CC   therapeutic (DITHP) polypeptides (II), which include e.g. enzymes, and
CC   proteins involved in growth and development and receptors. (I) and (II)
CC   may be used in the prevention, diagnosis and treatment of diseases
CC   associated with inappropriate DITHP expression. For example, (I) and (II)
CC   may be used to treat disorders associated with decreased polypeptide
CC   expression by rectifying mutations or deletions in a patient's genome,
CC   that affect the activity of the DITHPs, by expressing inactive proteins
CC   or supplementing the patient's own production of them. (I) and (II) may
CC   be used to treat diseases, for example, cell proliferative disorder,
CC   Crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma,
CC   leukaemia, autoimmune disorders, and respiratory disorders. Additionally,
CC   (I) may be used to produce the DITHPs, by inserting the nucleic acids
CC   into a host cell and culturing the cell to express the protein. (I) and
CC   its complementary sequences may also be used as DNA probes in diagnostic
CC   assays to detect and quantitate the presence of similar nucleic acids in
CC   samples, and therefore which patients may be in need of restorative
CC   therapy. (II) may also be used as antigens in the production of
CC   antibodies against DITHPs and in assays to identify modulators of DITHP
CC   expression and activity. The anti-DITHP antibodies and antagonists may
CC   also be used to down regulate expression and activity. The anti-DITHP
CC   antibodies may also be used as diagnostic agents for detecting the
CC   presence of DITHPs in samples (e.g. by enzyme linked immunosorbant assay
```

```
CC   (ELISA)). AAU19415-AAU19625 represent human diagnostic and therapeutic
CC   (DITHP) polypeptides of the invention
XX
SQ   Sequence 757 AA;

  Query Match             56.0%;  Score 1027.5;  DB 4;  Length 757;
  Best Local Similarity   59.1%;  Pred. No. 5.1e-92;
  Matches  212;  Conservative   50;  Mismatches   84;  Indels   13;  Gaps    6;

Qy          3 GGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAF 62
              |   :|| ||:|| | || |   ||:| :: |: || |      |    |:     || |
Db         17 GDSKVKVAVRIRPMNRRETDLHTKCVVDVDANKVILNPVNTNLSKGDARGQ-----PKVF 71

Qy         63 AFDRSYWSFDKNA-PNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGY 121
              |:|  :|| |::    || |: :|: ||  :| ||| ||| ||||||||||||||:|||
Db         72 AYDHCFWSMDESVKEKYAGQDIVFKCLGENILQNAFDGYNACIFAYGQTGSGKSYTMMGT 131

Qy        122 GKEHGVIPRICQDMFRRINELQKDKN--LTCTVEVSYLEIYNERVRDLLNP-STKGNLKV 178
               : |:|||:|  :| |    ||::|   :  |||||:|||||:|||||:|  ::  |||
Db        132 ADQPGLIPRLCSGLFER---TQKEENEEQSFKVEVSYMEIYNEKVRDLLDPKGSRQTLKV 188

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
              |||   |||| |:|| | |:::||:|| ||||:|||||||||| |||||||| :|||
Db        189 REHSVLGPYVDGLSKLAVTSYKDIESLMSEGNKSRTVAATNMNEESSRSHAVFKITLTHT 248

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
               :| ::    ||| |:|||||||||||| ||| | |||||: ||:||:||| ||:||||
Db        249 LYDVKSGTSGEKVGKLSLVDLAGSERATKTGAAGDRLKEGSNINKSLTTLGLVISALADQ 308

Qy        299 SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK 357
              |:||  ||: |||||||||||||||||||| |||:| :|||  |::|||||||||| ||
Db        309 SAGK-NKNKFVPYRDSVLTWLLKDSLGGNSKTAMVATVSPAADNYDETLSTLRYADRAK 366


RESULT 27
ABP51294
ID   ABP51294 standard; protein; 757 AA.
XX
AC   ABP51294;
XX
DT   03-SEP-2002  (first entry)
XX
DE   Human MDDT SEQ ID NO 316.
XX
KW   Human; MDDT; disease detection and treatment molecule polynucleotide;
KW   proliferative disorder; hepatitis; psoriasis; cancer; AIDS;
KW   autoimmune disorder; inflammatory disorder; allergy; multiple sclerosis;
KW   rheumatoid arthritis; transgenic; gene therapy; antiarteriosclerotic;
KW   hepatotropic; antiinflammatory; antipsoriatic; cytostatic; anti-HIV;
KW   antiallergic; antianaemic; antiasthmatic; antiatherosclerotic; antigout;
KW   neuroprotective; antirheumatic; antiarthritic.
XX
OS   Homo sapiens.
XX
PN   WO200240715-A2.
XX
PD   23-MAY-2002.
XX
PF   06-SEP-2001; 2001WO-US027628.
XX
PR   05-SEP-2000; 2000US-0229747P.
PR   05-SEP-2000; 2000US-0229748P.
PR   05-SEP-2000; 2000US-0229749P.
PR   05-SEP-2000; 2000US-0229750P.
PR   05-SEP-2000; 2000US-0229751P.
PR   05-SEP-2000; 2000US-0230583P.
PR   06-SEP-2000; 2000US-0230505P.
PR   06-SEP-2000; 2000US-0230514P.
PR   06-SEP-2000; 2000US-0230515P.
PR   06-SEP-2000; 2000US-0230517P.
PR   06-SEP-2000; 2000US-0230518P.
PR   06-SEP-2000; 2000US-0230519P.
PR   06-SEP-2000; 2000US-0230595P.
PR   06-SEP-2000; 2000US-0230597P.
PR   06-SEP-2000; 2000US-0230598P.
PR   06-SEP-2000; 2000US-0230599P.
PR   06-SEP-2000; 2000US-0230610P.
PR   06-SEP-2000; 2000US-0230865P.
PR   06-SEP-2000; 2000US-0230988P.
PR   06-SEP-2000; 2000US-0230989P.
PR   07-SEP-2000; 2000US-0230951P.
PR   07-SEP-2000; 2000US-0231163P.
PR   07-SEP-2000; 2000US-0231167P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Jackson S,  Lincoln SE,  Altus CM,  Dufour GE,  Chalup MS;
PI   Hillman JL,  Jones AL,  Yu JY,  Wright RJ,  Gietzen D,  Liu TF,  Yap PE;
PI   Dahl CR,  Momiyama MG,  Bradley DL,  Rohatgi SD,  Harris B;
PI   Roseberry AM,  Gerstin EH,  Peralta CH,  David MH,  Panzer SR,  Flores V;
PI   Daffo A,  Marwaha R,  Chen AJ,  Chang SC,  Au AP,  Inman RR;
XX
DR   WPI; 2002-527544/56.
DR   N-PSDB; ABQ72512.
XX
PT   Novel human disease detection and treatment polypeptide, useful in
PT   diagnosis, prevention or treatment of cell proliferative disorders e.g.
PT   arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder e.g.
PT   AIDS.
XX
PS   Claim 14; Page 485-486; 618pp; English.
XX
CC   The invention relates to an isolated human disease detection and
CC   treatment (MDDT) polypeptide (I) selected from a polypeptide having a
CC   sequence selected from 254 sequences (ABP51231-ABP51484) given in the
CC   specification, a naturally occurring polypeptide comprising a sequence
CC   having at least 90% identity to (I) or a biologically active or
CC   immunogenic fragment of (I). (I) is useful for screening a compound for
CC   effectiveness as an agonist or antagonist, for screening a compound that
CC   specifically binds (I) or modulates the activity of (I), and for
CC   preparing a polyclonal or monoclonal antibody by hybridoma technology.
CC   Nucleic acids (II) (ABQ72449-ABQ72700) encoding (I) are useful for
CC   screening a compound for effectiveness in altering expression of a target
CC   polynucleotide comprising. Oligonucleotides and antibodies are useful for
CC   detecting MDDT in a sample or for assessing toxicity of a test compound,
CC   in a diagnostic test for a condition or a disease associated with the
CC   expression of MDDT in a biological sample, for detecting (I) in a sample,
CC   and for purifying (I) from a sample. A composition comprising (I), an
CC   agonist or antagonist is useful for treating a disease or condition
CC   associated with decreased or increased expression of functional MDDT. (I)
CC   or (II) are useful for diagnosing, treating or preventing disorders
CC   associated with aberrant expression of MDDT, where the disorders are
CC   selected from a cell proliferative disorder such as arteriosclerosis,
CC   cirrhosis, hepatitis, psoriasis, and cancer and an
CC   autoimmune/inflammatory disorder such as AIDS, Addison's disease,
CC   allergy, anaemia, asthma, atherosclerosis, gout, multiple sclerosis or
CC   rheumatoid arthritis. (II) are useful for creating knockin humanised
CC   animals or transgenic animals to model human diseases, in somatic or
CC   germline gene therapy, to generate a transcript image of a tissue or cell
CC   type, for detecting differences in the chromosomal location due to
CC   translocation or inversion among normal, carrier or affected individuals
CC   and as hybridisation probes for mapping naturally occurring genomic
CC   sequences
XX
SQ   Sequence 757 AA;

  Query Match             56.0%;  Score 1027.5;  DB 5;  Length 757;
  Best Local Similarity   59.1%;  Pred. No. 5.1e-92;
  Matches  212;  Conservative   50;  Mismatches   84;  Indels   13;  Gaps    6;

Qy          3 GGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAF 62
              |   :|| ||:|| | || |   ||:| :: |: || |      |    |:     || |
Db         17 GDSKVKVAVRIRPMNRRETDLHTKCVVDVDANKVILNPVNTNLSKGDARGQ-----PKVF 71

Qy         63 AFDRSYWSFDKNA-PNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGY 121
              |:|  :|| |::    || |: :|: ||  :| ||| ||| ||||||||||||||:|||
```

```
Db         72 AYDHCFWSMDESVKEKYAGQDIVFKCLGENILQNAFDGYNACIFAYGQTGSGKSYTMMGT 131

Qy        122 GKEHGVIPRICQDMFRRINELQKDKN--LTCTVEVSYLEIYNERVRDLLNP-STKGNLKV 178
                : |:|||:|  :| |    ||::|   :  |||||:|||||:|||||:|  ::  |||
Db        132 ADQPGLIPRLCSGLFER---TQKEENEEQSFKVEVSYMEIYNEKVRDLLDPKGSRQTLKV 188

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
             |||   ||||: |:|| | |:::||:|| ||||:|||||||||| ||||||| :|||
Db        189 REHSVLGPYVDGLSKLAVTSYKDIESLMSEGNKSRTVAATNMNEESSRSHAVFKITLTHT 248

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
              :| ::    ||| |:|||||||||||| ||| | |||||: ||:||:||| ||:||||
Db        249 LYDVKSGTSGEKVGKLSLVDLAGSERATKTGAAGDRLKEGSNINKSLTTLGLVISALADQ 308

Qy        299 SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK 357
             |:||  ||: |||||||||||||||||||| |||:| :|||  |::|||||||||| ||
Db        309 SAGK-NKNKFVPYRDSVLTWLLKDSLGGNSKTAMVATVSPAADNYDETLSTLRYADRAK 366


RESULT 28
ABG60124
ID   ABG60124 standard; protein; 762 AA.
XX
AC   ABG60124;
XX
DT   30-JUL-2002  (first entry)
XX
DE   Human DITHP polypeptide #182.
XX
KW   Human; DITHP; diagnostic and therapeutic polypeptide; bone; testis; skin;
KW   cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;
KW   inflammatory disorder; viral infection; bacterial infection; seizure;
KW   fungal infection; parasitic infections; developmental disorder; breast;
KW   endocrine disorder; metabolic disorder; neurological disorder; cervix;
KW   gastrointestinal disorder; transport disorder; gene therapy; kidney;
KW   adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
KW   thymus.
XX
OS   Homo sapiens.
XX
PN   WO200220754-A2.
XX
PD   14-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US027127.
XX
PR   05-SEP-2000; 2000US-0229747P.
PR   05-SEP-2000; 2000US-0229748P.
PR   05-SEP-2000; 2000US-0229749P.
PR   05-SEP-2000; 2000US-0229750P.
PR   05-SEP-2000; 2000US-0229751P.
PR   05-SEP-2000; 2000US-0230583P.
PR   06-SEP-2000; 2000US-0230505P.
PR   06-SEP-2000; 2000US-0230514P.
PR   06-SEP-2000; 2000US-0230515P.
PR   06-SEP-2000; 2000US-0230517P.
PR   06-SEP-2000; 2000US-0230518P.
PR   06-SEP-2000; 2000US-0230519P.
PR   06-SEP-2000; 2000US-0230595P.
PR   06-SEP-2000; 2000US-0230597P.
PR   06-SEP-2000; 2000US-0230598P.
PR   06-SEP-2000; 2000US-0230599P.
PR   06-SEP-2000; 2000US-0230610P.
PR   06-SEP-2000; 2000US-0230865P.
PR   06-SEP-2000; 2000US-0230988P.
PR   07-SEP-2000; 2000US-0230951P.
PR   07-SEP-2000; 2000US-0231163P.
PR   07-SEP-2000; 2000US-0231167P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Stuart J,  Lincoln SE,  Altus CM,  Dufour GE,  Chalup MS,  Hillman JL;
PI   Jones AL,  Yu JY,  Wright RJ,  Gietzen D,  Liu TF,  Yap PE,  Dahl CR;
PI   Momiyama MG,  Bradley DL,  Rohatgi SD,  Harris B,  Roseberry AM;
PI   Gerstin EH,  Peralta CH,  David MH,  Panzer SR,  Flores V,  Daffo A;
PI   Marwaha R,  Chen AJ,  Chang SC,  Au AP,  Inman RR;
XX
DR   WPI; 2002-383054/41.
DR   N-PSDB; ABK71715.
XX
PT   An isolated polynucleotide useful in diagnostics and therapeutics.
XX
PS   Claim 29; Page 637-639; 686pp; English.
XX
CC   The invention relates to human diagnostic and therapeutic (dithp)
CC   polynucleotides and their associated polypeptides (DITHP polypeptides).
CC   The sequences of the invention are used in the treatment and diagnosis of
CC   cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
CC   (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast,
CC   cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or
CC   thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,
CC   psoriasis, osteoporosis), viral infections, bacterial infections, fungal
CC   infections, parasitic infections, developmental disorders (e.g. anaemia,
CC   epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),
CC   endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders
CC   (e.g. obesity, diabetes), neurological disorders (e.g. stroke,
CC   amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal
CC   disorders (e.g. ulcerative colitis, lysinuria) and transport disorders
CC   (e.g. myotonic dystrophy, catatonia, peripheral neuropathy). Sequences
CC   ABG59943-ABG60220 represent human DITHP polypeptides of the invention
XX
SQ   Sequence 762 AA;

  Query Match             55.6%;  Score 1020.5;  DB 5;  Length 762;
  Best Local Similarity   58.8%;  Pred. No. 2.6e-91;
  Matches  211;  Conservative   50;  Mismatches   85;  Indels   13;  Gaps    6;

Qy          3 GGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAF 62
              |   :|| ||:|| | || |   ||:| :: |: || |       |    |:     || |
Db         17 GDSKVKVAVRIRPMNRRETDLHTKCVVDVDANKVILNPVNTNLSKGDARGQ-----PKVF 71

Qy         63 AFDRSYWSFDKNA-PNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGY 121
              |:|  :|| |::    || |: :|: ||  :| ||| ||| ||||||||||||||:||
Db         72 AYDHCFWSMDESVKEKYAGQDIVFKCLGENILQNAFDGYNACIFAYGQTGSGKSYTMMGT 131

Qy        122 GKEHGVIPRICQDMFRRINELQKDKN--LTCTVEVSYLEIYNERVRDLLNP-STKGNLKV 178
                : |:|||:|  :| |    ||::|   :  |||||:|||||:|||||:|  ::  |||
Db        132 ADQPGLIPRLCSGLFER---TQKEENEEQSFKVEVSYMEIYNEKVRDLLDPKGSRQTLKV 188

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
             |||   ||||: |:|| | |:::||:|| ||||:|||||||||| ||||||| :|||
Db        189 REHSVLGPYVDGLSKLAVTSYKDIESLMSEGNKSRTVAATNMNEESSRSHAVFKITLTHT 248

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
              :| ::    ||| |:|||||||||||| ||| | |||||: ||:||:||  ||:||||
Db        249 LYDVKSGTSGEKVGKLSLVDLAGSERATKTGAAGDRLKEGSNINKSLTTLDLVISALADQ 308

Qy        299 SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK 357
             |:||  ||: |||||||||||||||||||| |||:| :|||  |::|||||||||| ||
Db        309 SAGK-NKNKFVPYRDSVLTWLLKDSLGGNSKTAMVATVSPAADNYDETLSTLRYADRAK 366


RESULT 29
ADJ69671
ID   ADJ69671 standard; protein; 1826 AA.
XX
AC   ADJ69671;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human heat mitochondrial protein as a therapeutic target SeqID1477.
XX
KW   mitochondrial; human; screening assay; diabetes mellitus;
KW   Huntington's disease; osteoarthritis;
KW   Leber's hereditary optic neuropathy; LHON;
KW   mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
```

KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX
DR WPI; 2003-845369/78.
XX
PT Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
PS Claim 1; SEQ ID NO 1477; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 1826 AA;

Query Match 55.4%; Score 1016.5; DB 7; Length 1826;
Best Local Similarity 58.5%; Pred. No. 2.7e-90;
Matches 210; Conservative 49; Mismatches 87; Indels 13; Gaps 6;

```
Qy          3 GGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAF 62
              |   :|| ||:|| | || |   ||:| :: |: || |       |    |:     || |
Db          2 GDSKVKVAVRIRPMNRRETDLHTKCVVDVDANKVILNPVNTNLSKGDARGQ-----PKCF 56

Qy         63 AFDRSYWSFDKNA-PNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGY 121
              |:|  :|| |::    || |: :|: ||  :| ||| ||| ||||||||||||||:|||
Db         57 AYDHCFWSMDESVKEKYAGQDIVFKCLGENILQNAFDGYNACIFAYGQTGSGKSYTMMGT 116

Qy        122 GKEHGVIPRICQDMFRRINELQKDKN--LTCTVEVSYLEIYNERVRDLLNP-STKGNLKV 178
                : |:|||:|  :| |   ||::|   :  |||||:|||||:|||||:|  ::  |||
Db        117 ADQPGLIPRLCSGLFER---TQKEENEEQSFKVEVSYMEIYNEKVRDLLDPKGSRQTLKV 173

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
              |||   ||||: |:||   |:::||:|| ||||:||||||||| |||||||  :|||
Db        174 REHSVLGPYVDGLSKLAATSYKDIESLMSEGNKSRTVAATNMNEESSRSHAVLKITLTHT 233

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
               :| ::    ||| |:||||||||||| ||| | ||||| || ||:||| ||:||||
Db        234 LYDAKSGTSGEKVGKLSLVDLAGSERATKTGAAGDRLKEGSNINESLTTLGLVISALADQ 293

Qy        299 SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK 357
              |:||  ||: |||||||||||||||||||| |||:| :|||  |::|||||||| ||
Db        294 SAGK-NKNKFVPYRDSVLTWLLKDSLGGNSKTAMVATVSPAADNYDETLSTLRYADRAK 351
```

RESULT 30
ADL83235
ID ADL83235 standard; protein; 1826 AA.
XX
AC ADL83235;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human PRO60891, SEQ ID 437.
XX
KW Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
KW Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
KW Gene Therapy; PRO; B cell related disorder; cancer;
KW immune-mediated inflammatory disease; human.
XX
OS Homo sapiens.
XX
PN WO2004024097-A2.
XX
PD 25-MAR-2004.
XX
PF 15-SEP-2003; 2003WO-US029097.
XX
PR 16-SEP-2002; 2002US-0411392P.
XX
PA (GETH) GENENTECH INC.
XX
PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
PI Wu TD;
XX
DR WPI; 2004-329389/30.
DR N-PSDB; ADL83234.
XX
PT New PRO polypeptide, useful for diagnosing and treating a B cell related
PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
XX
PS Claim 10; Fig 437; 695pp; English.
XX
CC The present invention relates to PRO proteins and their coding sequences.
CC The PRO proteins are useful for diagnosing and treating a B cell related
CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
CC antigen unresponsiveness, selective IgA deficiency, selective IgM
CC deficiency, selective deficiency of IgG subclasses, immunodeficiency with
CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
CC lymphoma, intermediate lymphoma, follicular lymphoma, type II
CC hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic
CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
CC ankylosing spondylitis. The PRO proteins are also useful for preparing a
CC medicament for treating a condition that is responsive to the PRO
CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
CC coding sequences are useful as hybridization probes in chromosome and
CC gene mapping, in preparing PRO proteins, or in generating transgenic
CC animals or knockout animals, which in turn are useful in the development
CC and screening of therapeutically useful reagents.
XX
SQ Sequence 1826 AA;

Query Match 55.4%; Score 1016.5; DB 8; Length 1826;
Best Local Similarity 58.5%; Pred. No. 2.7e-90;
Matches 210; Conservative 49; Mismatches 87; Indels 13; Gaps 6;

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Qy          3 GGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAF 62
              |   :|| ||:|| | || |   ||:| :: |: || |       |    |:     || |
Db          2 GDSKVKVAVRIRPMNRRETDLHTKCVVDVDANKVILNPVNTNLSKGDARGQ-----PKCF 56

Qy         63 AFDRSYWSFDKNA-PNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGY 121
              |:|  :|| |::    || |: :|: ||  :| ||| ||| ||||||||||||||:|||
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Db         57 AYDHCFWSMDESVKEKYAGQDIVFKCLGENILQNAFDGYNACIFAYGQTGSGKSYTMMGT 116

Qy        122 GKEHGVIPRICQDMFRRINELQKDKN--LTCTVEVSYLEIYNERVRDLLNP-STKGNLKV 178

Db        117 ADQPGLIPRLCSGLFER---TQKEENEEQSFKVEVSYMEIYNEKVRDLLDPKGSRQTLKV 173

Qy        179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238

Db        174 REHSVLGPYVDGLSKLAATSYKDIESLMSEGNKSRTVAATNMNEESSRSHAVLKITLTHT 233

Qy        239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298

Db        234 LYDAKSGTSGEKVGKLSLVDLAGSERATKTGAAGDRLKEGSNINESLTTLGLVISALADQ 293

Qy        299 SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK 357

Db        294 SAGK-NKNKFVPYRDSVLTWLLKDSLGGNSKTAMVATVSPAADNYDETLSTLRYADRAK 351


Search completed: September 5, 2006, 18:04:43
Job time : 201 secs
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